

Best Local Similarity 84.2%; Pred. No. 4.3e-66;
Matches 529; Conservative 0; Mismatches 0

[illegible]

RESULT	6
Accession	AJ798934/c
LOCUS	
DEFINITION	AI798934 w94e04.xl Soares_NFL_T_OBC.SI Homo sapiens cdna clone IMAGE:2348766 3' similar to SW:I132_HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2 CHAIN PRECURSOR ; mRNA sequence.
ACCESSION	.AJ798934
VERSION	AI798934.1 GI:5364406
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
TITLE	unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: cgapsb@mail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 882 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 468.

FEATURES

FEATURES	source
Location/Qualifiers	1. .676
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:2348766"	
/clone_lib="Soares_NFL_T_GBC_S1"	
/lab_host="DH10B"	
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NHL19W, testis NWT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, and ss circles were used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."	205 a 133 c 117 g 221 c
BASE COUNT	
ORIGIN	

Query Match	26.7%	Score 387.8	DB 9	Length 676
Best Local Similarity	76.5%	Pred. No. 1.7e-57		
Matches 518	Conservative 0	Mismatches 147	Indels 12	Gaps 3
QY 754	ggaaaaatatggatgcaggtttccctattgttgatcattcagacattataaagattttctac	813		
DB 676	GGACACAATATAGGATGCAGATTTCCCTATTTTGGAGCATCAGACTATAGAGATATCTAT	617		
QY 814	atctgtgttaatgggtcatcaagaatccagcctatcagaccagctattttttttttcag	873		
DB 616	ATTGTGTAAATGGATCATCAGAGAAGCAGCTATCAGATCCAGTTATTTCACTTGTCTAG	557		
QY 874	cttcaaaatagttaaacctatgcaccagactacotttagtcttactctgtaagaattcca	933		
DB 556	CTTCAAAATATAGTTAAACCTTTGCCGCCAGTCTATCTTACTTTTACTCGGGAGAGTTCA	497		
QY 934	gaggaaattaacctgaaatggaaatgcctaaaggaccattccagccgaataatttttcatt	993		
DB 496	TGTCAAATTAAAGCTGAATGGAGCATACCTTTGGGACCTATTCCAGCAAGGTTTTTGAT	437		
QY 994	tatgaattgaattcacagaggatggtactacttgggtgactaccacagctgagaaatgag	1053		
DB 436	TATGAAATTGAGATCAGAGAAGATGATACCACCTTGGTACTCTACAGTTGAAATGAA	377		
QY 1054	atacaatcacagaacaatcaaatgaaagccaaataattgcttttttggtaagaagtcaa	1113		
DB 376	ACATACACCTTTGAAACACAAATGAACCCGCAATATTGCTTTGTAGTAAGAAGCAA	317		
QY 1114	gtgaattttattgttcagatgatgaaatctggagtgagtgagtgatgaacaatgtcg	1173		
DB 316	GTCAATATTATTTCACAGATGCGGAAATTTGGAGTGTGGAGTGATAAACAATGCTGG	257		
QY 1174	aaaggtg---acatatggaagaaaccttagtatattttcttataccatttgcctttgtc	1230		
DB 256	GAAGGTGAAACCTATCGAAGAAACTTTGCTACGGTTTCTGGCTACCAATTTGGTTTCATC	197		
QY 1231	tcaatttgttttggtaataacttgcctgttttggtaagaagaagggctttactaggaa	1290		
DB 196	TTAATATTAGTTATATTGTAACCGGTCTGCTTTTTCGGTAGCCAAACCCCTTACC	137		
QY 1291	acgat-----ctttcatacaaaaaagaagctttttctcatcagaacacattctgtg	1343		
DB 136	ATGATTCACAGAAATTTTCTGTATACATGAAGACTTTCCATATCAAGAGACATGGTATTG	77		
QY 1344	actcagtaacttcagttcttatggccagatgttaaatatgagtcttataaactgaaagt	1403		
DB 76	ACTCAACAGTTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATRAACHTGA	19		
QY 1404	ttctctcaaatattgaa 1420			

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/dev_stage="7 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

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BASE COUNT      186 a  119 c  146 g  198 t
ORIGIN

Query Match      18.7%; Score 271.2; DB 10; Length 649;
Best Local Similarity 72.9%; Pred. No. 2.2e-37;
Matches 411; Conservative 0; Mismatches 133; Indels 20; Gaps 4;

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Qy 39 gaagggaagcttagagattctaataatgtctccaaactgagagagaaaaaagag 98
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GAAGGAAACAGTAGAGAGTCAATTTAGTGCT-----AATGTGGAAAGGACAGAGAG 56
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 99 gacctgtgataattgcctatgataattcattcttgagaaccattattgagtgga 158
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 GTCITGTGTAACCTGCTGATATACATTTCTTGAGAACCATATTTAGTAGAGC 116
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 159 cttcaagaattgaactgtgagggaatgcttccattcatttggtgcggaattcctcta 218
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117 TTTGAGCACACTAAATCTCGGAAATGGCTTT-----TGTCATATCAGATGCTTGTG 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 219 taccctgtcttgacagacattggtctctatgcttccaaatgctgagataaaagttaa 278
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 171 TTTCAATCTCTTTGTACAAATAACTGGCTAT-----TCTTTGGAGATAAAAGTTAA 221
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 279 tcctctcaggatttgtagatgtagacctggatattagttatctctctcttgcgaatg 338
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 222 TCCCTCTCAGGATTTGAAATATTCGATTCCTGGATATTGTTATCTCTATTTCCATG 281
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 339 gcaacctccattatttccgggataattttaaggaatgcacaaatagaatgaattaaaata 398
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 282 GAAACCTCTCTGGTTATAGAAAATTTAAGGGCTGTACACTAGATAATGAGTTAAATA 341
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 399 ccgaaacattagatgaaactggaagaccatcattaccagaatctacattacaaga 458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 342 CCGAAATTTGATACGACAGCTGGAAGACTATAATTACTAGGAATCTAATTTTCAAGGA 401
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 459 tgggttgatcttaacaaagtattgaagcaagaataacacactctgccagcacaatg 518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 402 TGGTTTGATCTTATAAGGCATTAAGGAAGATACGTAAGCATTGTCAGACCATG 461
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 519 cacaatatgga-tcagaagttagaagttcattgggagaaactacttattggacatcacac 577
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 462 TACCACGTGACTCAGAGTCAACCAAGTCCATGATCGAAGCTCTTATGGACTCTCCGAT 521
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 578 aaggaaatcgaggaaactaaaattc 601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 522 GAAGGAGTTTGGAAACTCAATTC 545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

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RESULT 14
AA298563
LOCUS      EST114178 HSC172 cells I Homo sapiens cDNA 5' end similar to IL13
DEFINITION receptor (IL13R), mRNA sequence.
ACCESSION AA298563
VERSION   AA298563.1 GI:1950896
KEYWORDS  EST.
SOURCE    human.
ORGANISM Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 365)
AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
            ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
            ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

```

RESULT
13661

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Pelligrino,S.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrle,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

96026280
Other_ESTs: THC194124
Contact: Kerlavage, AR

Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
source
1..365
/organism="Homo sapiens"
/db_xref="ATCC (Inhost):178283"
/db_xref="taxon:9606"
/clone_lib="HSC172 cells I"
/cell_type="fibroblast"
/cell_line="HSC172 (16PDL)"
/dev_stage="fetal"
/note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
; Site_2: XhoI"

BASE COUNT 106 a 66 c 69 g 123 t 1 others
ORIGIN

Query Match 18.2%; Score 264.4; DB 9; Length 365;
Best Local Similarity 86.3%; Pred. No. 4e-36;
Matches 303; Conservative 0; Mismatches 47; Indels 1; Gaps 1;

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Qy 563 attggacatcaccacaaggaatcggaactaaattcaagatatgactgtgtatatt 622
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Db 1 ATTTGATATACCAAGGAATTCAGAAACTAAAGTTCAGGATATGATGCGTATTATT 60
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Qy 623 acaactggcaatatttagctgtctcttggaaacctggcatgggtgtccattttgatacca 682
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ACAATTGGCAATATTACTCTGTTCTTGGAAACCTGGCATAGGTCTACTTCTTGATACCA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 683 attaccagttgttttactggtatgagggcttggaccattcagcagagtgactgattaca 742
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ATTACAACCTTTTACTTGGTATGAGGGCTTGGTTTCATGTCATACAGTGTGTGATTACA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 743 tcaagggttaatggaaaaaatatggatgcaggtttccctattttgagtcacagactata 802
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 TCAAGGCTGATGGACAAATATAGATATAGATTTCCTTATTTGGAGCATCAGACTATA 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 803 aagatttcacatctgttttaattggtgtcatcagaatccagcctcatcagacccagctatt 862
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 AAGATTCTTATATTGTGTTAATGGATCATCAGAGANCAAGCTCATCAGATCCAGTTATT 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 863 tta-tttttcaggttcaaaatagtttaaacctatgcccacagactacctt 912
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TCACCTTTCCAGCTTCAAAATATAGTTAAACCTTTTGGCGGCGAGTCTATCCT 351
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 10:52:12 : Search time 4150.53 Seconds
(without alignments)
2016.155 Million cell updates/sec

Title: US-09-828-995B-54
Perfect score: 620
Sequence: 1 ggcacgagctgagtgttg.....caagatatggactgtgtata 620

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : EST.*
- 1: em_estba.*
 - 2: em_esthum.*
 - 3: em_estin.*
 - 4: em_estnu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_htc.*
 - 9: gb_est1.*
 - 10: gb_est2.*
 - 11: gb_htc.*
 - 12: gb_gss.*
 - 13: em_gss_hum.*
 - 14: em_gss_inv.*
 - 15: em_gss_pln.*
 - 16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	341.2	55.0	954	9	AL525497
2	336.6	54.3	683	10	BG778615
3	328.2	52.9	743	10	BG723203
4	323.2	52.1	658	10	B1828427
5	271.2	43.7	649	10	BE289033
6	261.4	42.2	476	10	BF443846
7	248	40.0	379	10	BF443844
8	192.4	31.0	473	10	R52795
9	188.6	30.4	928	9	AL562513
10	188.2	30.4	904	10	B1462644
11	142.4	23.0	715	10	BE788633
12	116.6	18.8	755	10	BE619361
13	49.6	8.0	942	12	CNS018GS
14	45.4	7.3	1101	12	CNS0039G
15	45.2	7.3	365	9	AA298563
16	45.2	7.3	840	12	BH153955
17	44.6	7.2	1101	12	CNS0039G

C 18	44	7.1	1001	12	CNS0064G
C 19	43.2	7.0	791	12	AQ865293
C 20	43	6.9	641	12	AZ523481
C 21	43	6.9	645	12	AZ522162
C 22	42.8	6.9	704	10	BM163666
C 23	42.8	6.9	879	12	AZ678808
C 24	42.6	6.9	579	12	CNS00F20
C 25	42.6	6.9	639	12	CNS017QD
C 26	42.6	6.9	903	12	CNS00I1C
C 27	42.4	6.8	481	9	AW305472
C 28	42.4	6.8	513	9	AL516344
C 29	42.4	6.8	549	12	CNS0248Y
C 30	42.4	6.8	677	12	B89641
C 31	42.4	6.8	1013	9	AL564621
C 32	42.2	6.8	928	10	BF274633
C 33	42.2	6.8	1025	12	CNS014J2
C 34	42	6.8	984	12	CNS01POS
C 35	41.8	6.7	438	12	AQ132259
C 36	41.8	6.7	928	12	CNS06DH6
C 37	41.4	6.7	1223	12	B12981
C 38	41.2	6.6	982	12	CNS006BE
C 39	41	6.6	461	12	B67180
C 40	41	6.6	908	12	BH138952
C 41	40.8	6.6	390	12	AQ125679
C 42	40.8	6.6	1101	12	CNS000NX
C 43	40.6	6.5	812	12	CNS00IDC
C 44	40.6	6.5	928	12	CNS00DKY
C 45	40.6	6.5	998	12	AZ680790

ALIGNMENTS

RESULT 1
AL525497 954 bp mRNA linear EST I3-FEB-2001
LOCUS LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC012YF21 5
DEFINITION prime, mRNA sequence.
ACCESSION AL525497
VERSION AL525497.1 GI:12788990
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 954)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .954
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC012YF21"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

FEATURES

source
295 a 172 c 201 g 285 t 1 others
BASE COUNT

ORIGIN

Query Match 55.0%; Score 341.2; DB 9; Length 954;
Best Local Similarity 84.0%; Pred. No. 1.5e-67;
Matches 398; Conservative 0; Mismatches 73; Indels 3; Gaps 1;
Qy 150 gagtggaaactcaagattgaattcttggaggaatggtcttcattcatttggatgctgg 209
Db 44 GAGAGCAATATCAAGGTTTAAATCTCGGAGAAATGGCTTTCGTTTGGCTGATCGG 103
Qy 210 attctctatataccctctgttggtaagcagcatttggct---ctatgcttttcaaatgctga 266
Db 104 ATGCTTATATACCTTCTGATGAAGCACAAACATTTGGCTGTACTTTCATCTTCAGACCGGA 163
Qy 267 gataaaagttaactctctcctcaggttttggatgtagtagcaccctgagatttaggttatct 326
Db 164 GATAAAAGTTAACTCTCTCAGATTTTGAGATAGTGGATCCGGATACTTAGGTTATCT 223
Qy 327 ctcttggcaatggcaacctccattatttccggataattttaaagggaatgcacataagaata 386
Db 224 CTATTTGCAATGGCAACCCCACTCTCTGGATCATTTTAAGGAATGCACAGTGAATA 283
Qy 387 tgaataaaataccgaacatgtagtgaataactcgggaagaccatcattaccagaatct 446
Db 284 TGAACATAAATACCGAAACATTTGGTAGTGAAACATGGAGACCATCATTTACTTAAGAATCT 343
Qy 447 acattacaaagtgtgtgtatcttaeaaagggtatttgaagcaaaagataaaacacacttct 506
Db 344 ACATTTACAAAGATGGTTTGATCTTTAACAGGGCAATTAAGGCAAGATACACACGCTTTT 403
Qy 507 gccagcaaatgcacaaatggatcagaagtagtagaagttcatggggcagaaactactattg 566
Db 404 ACCATGGCAATGCACAAATGGATCAGAGTTCAAAGTTCTCTGGGAGAACTACTTATTG 463
Qy 567 gacatcacacaagaatcggggaactaaataattcaagatatggctgtgata 620
Db 464 GATATCACCACAAAGAAATTCAGAAACTAAAGTTCCAGGATATGGATTGGGTATA 517

RESULT 2

LOCUS BG778615 683 bp mRNA linear EST 15-MAY-2001
DEFINITION 602668073F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4807603 5',
mRNA sequence.

ACCESSION BG778615

VERSION BG778615.1 GI:14048932

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 683)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DP

cDNA Library Preparation: CLONETECH Laboratories, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LicM1659 row: b column: 20

High quality sequence stop: 683.

Location/Qualifiers

1. 683

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4807603"

/clone_lib="NIH_MGC_60"

FEATURES

source

/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggcgctctggcc); Site_2: Sfil (ggcatatggcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGAGCGGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."

BASE COUNT 212 a 124 c 140 g 207 t

ORIGIN

Query Match 54.3%; Score 336.6; DB 10; Length 683;
Best Local Similarity 84.4%; Pred. No. 1.7e-66;
Matches 391; Conservative 0; Mismatches 69; Indels 3; Gaps 1;
Qy 161 tcaaaagtattgaattcttggaggaatggcttctcattcatttggatgtcggattcctctata 220
Db 4 TCAAGGTTTAAATCTCGGAGAAATGGCTTTCGTTTGGCTATCGGATGCTTATATA 63
Qy 221 cctctgttcttgcacagcatttggct---ctatgctttcaaatgctgagataaaagtta 277
Db 64 CTTTCTGTATAGCACACACATTTGGCTGTACTTCTTCACACACCGAGATAAAAGTTA 123
Qy 278 atctctctcaggaatttggatagtagtgacctggatatttaggttatctctcttctgcaat 337
Db 124 ACCCTCCTCAGGATTTTGAGATAGTGGATCCGGATACCTTAGTATCTCTATTTGCAAT 183
Qy 338 gcaacacctcattatttccggataattttaaagaaatgcacaaatagaatgaataaaat 397
Db 184 GGCAACCCCACTGTCTCTGGATCATTTTAAAGAAATGCACAGTGAATATGAACATAAAT 243
Qy 398 accgaaacattgatgtgaaactggaagaccatcattaccagaatctcacattacaag 457
Db 244 ACCGAAACATTTGGTAGTGAACATGGAAGACCATCATTTACTAAGATCTACATTACAAG 303
Qy 458 atgggtttgatcttaacaaaggtattgaagcaagaataaacacactcttgcagcagcaat 517
Db 304 ATGGGTTTGCATCTTAAAGGGCATTGAAGCGAAGATACACACGCTTTTACCATGGCAAT 363
Qy 518 gcacaaatggatcagaagtttagaagttcattggggcagaacaaactatttggacataccac 577
Db 364 GCACAAATGGATCAGAAAGTTCAAAGTTCTCTGGGAGAAACTACTTATTGGATATCACCAC 423
Qy 578 aaggaatcggaacataaaattcaagatatgactgtgtata 620
Db 424 AAGGAATTCAGAAACTAAAGTTCCAGGATATGGATTGGCTGATA 466

RESULT 3

LOCUS BG723203

DEFINITION 602690806F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4823185 5',
mRNA sequence.

ACCESSION BG723203

VERSION BG723203.1 GI:14002390

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 743)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM10732 row: 1 column: 02
 High quality sequence stop: 730.

FEATURES

source

1..743

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4823185"

/clone_lib="NIH_MGC_97"

/lab_host="DH10B"

/note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcggg
); Oligo-dT primed using primer 5'-tttttttttttttttVN-3',
 size-selected for average insert size 2.2 kb and
 normalized to R0T 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT

ORIGIN

229 a 135 c 164 g 214 t 1 others

Query Match

52.9%; Score 328.2; DB 10; Length 743;

Best Local Similarity 83.5%; Pred. No. 1.4e-64;

Matches 396; Conservative 0; Mismatches 74; Indels 4; Gaps 2;

Qy 150 gattggaacttcaagtattgaattcttgagggaatgctttcattcatttgatgtcgg 209

Db 49 GAGAGGCAATTAACGGTTTAAATCGGAGAAATGGCTTTCGTTGGCTATCGG 108

Qy 210 attctctatccctgctgtttgcacagcatttgct---ctatgcttcaaatgctga 266

Db 109 ATGCTTATACCTTCTGATAGCACACACATTTGGCTGTACTTCATCTTCAGACCGA 168

Qy 267 gataaagtttaactcctcctcaggattttgagatagtgagccctggatattaggttatct 326

Db 169 GATAAAGTTAAACCTCTCAGGA-TTTGAGATAGTGGATCCCGATACCTTAGGTTATCT 227

Qy 327 ctctttgcaatggcaacctccatttctccggataatttttaaggaatgcacaaatagaata 386

Db 228 CTATTTGCAATGGCAACCCCACTGCTCTGTGGATCATTTTAAAGGAATGCACAGTGAATA 287

Qy 387 tgaattaaaatcaccgaaacattgatagtgaaactggaagaccatcattaccagaatct 446

Db 288 TGAATAAATACCGAAACATTTGGTAGTGAACATGGNAGACCATCATTTACTAGATCT 347

Qy 447 acattcaaaagatgggttgatcttaacaaaggatttgaagcaagaataaacacacttct 506

Db 348 ACATTACAAAGATGGTTGATCTTAAACAGGGCATTGAAGCGAAGATACACACGCTTTT 407

Qy 507 gccagcaaatgcacaaatgatcagaagttagaagttcattcaggcagaacactatttg 566

Db 408 ACCATGCAATGGCAAAATGGATCAGAAAGTTCAAAGTTCTTCGGCAGAAATCTATTATNG 467

Qy 567 gacatccacaaaggaaatcggaactaaaattcaagatatgactgtgtata 620

Db 468 GATATCACCACAGGAATTCAGAAACTTAAGTTTCAGGATATGATGTCGRTATA 521

RESULT 4

B1828427

LOCUS

DEFINITION 603078385F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170268 5',

mRNA sequence.

ACCESSION

B1828427

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

B1828427.1 GI:15939977

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LHAM1423 row: i column: 21

High quality sequence stop: 651.

FEATURES

source

1..658

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5170268"

/clone_lib="NIH_MGC_119"

/tissue_type="medulla"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."

BASE COUNT

ORIGIN

202 a 121 c 141 g 194 t

Query Match

52.1%; Score 323.2; DB 10; Length 658;

Best Local Similarity 84.3%; Pred. No. 1.9e-63;

Matches 388; Conservative 0; Mismatches 68; Indels 4; Gaps 2;

Qy 164 aagattgaactcttgagggaatgctttcattcatttgatgtcggattcctctataacc 223

Db 28 AAGTTTAAATCTCGGAAATGGCTTTCGTTGGCTATCGGATGCTTATATACCT 87

Qy 224 tgcctgttgcacagcatttgct---ctatgcttcaaatgctgagataaaagttaac 280

Db 88 TTCTGATAAGCACACATTTGGCTGTACTTTCATCTTCAGACACCGAGATAAAGTTAAC 147

Qy 281 ctctcaggattttgagatagtgagccctggatattttaggttattctctcttgcattgac 340

Db 148 CTCCTCAGGA-TTTGAGATAGTGGATCCGGATACCTTAGGTTATCTCTATTATTGCAATG 206

Qy 341 aacctccatttccggataattttaaggaatgcacaaatagaataatgaataataacc 400

Db 207 AACCCCACTGCTCTGGATCATTTTAAAGGAATGCACAGTGGAAATATGAACATAAATACC 266

Qy 401 gaaacattgtagtgaactgggaagaccatcattaccagaatactacatacaagatg 460

Db 267 GAACATTGGTAGTGAACATGGGAAGACCACCATTTACCTAAGAACTCTACATTACAAGATG 326

Qy 461 gggttgatcttaacaaaggatttgaagcaaaagataaaacacacttctgcccacaaatgca 520

Db 327 GGTITGATCTTAAACAGGCGATTGAAGCGAAGATACACACGCTTTTACCATTGGCAATGCA 386

Qy 521 caaatggtatcgaagttagaagttcattggtgagaaactacttattggtacataccacaag 580

Db 387 CAAATGGATCAGAGTTCAAAGTTCTCTGGCAGAAACTACTTATTGGATATACCCACAAG 446


```
Qy 151 agtggaaactcaagattgaattcttgaggagaatggcttccattcattcattgagtcgga 210
|||||
Db 150 AGTGGAAACTTCAAGGTATTAAATCTTAGAGAAATGGCTTTATTTCATGTGAATATCAGA 209
|||||
Qy 211 ttcctctataacctgctgtgttggtgacagcatttggctcta---tgctttcaaatgctgag 267
|||||
Db 210 TGTCTATATAGTCTCTTATTATTGGCACAGCATTTGGCTCTACTTTGCTCTTCAAAATGCCGAG 269
|||||
Qy 268 ataaaagttaactcctcctcaggattttgagatagtggaacctggatatttaggttatctc 327
|||||
Db 270 ATAAAGTTAATCTCTCCACAGATTTGAATATAGTGGACCTGGATATTTAGGTATATCTC 329
|||||
Qy 328 tctttgcaatggcaacctccattatttcccggaataattttaaaggaaatgcacaaatgacat 387
|||||
Db 330 TATTGTGAGTGGCAACCTCCACTGCTCTGGATAAATTTAAGGAATGCACAGTAGAGTAT 389
|||||
Qy 388 gactttaaatacgaadattgagtaggaactggaagaccattacdaagaatcta 447
|||||
Db 390 GAATTAANAATACCGAAACATTGATAGTGAAGCTGGAAGACGATCATTTACTTAAGAATCTA 449
|||||
Qy 448 catlacdaagatgggtttgatctttaac 474
|||||
Db 450 CATTACAAAGATGGTTTGATCTTAAC 476
|||||

RESULT 7
LOCUS BF443844 379 bp mRNA linear EST 01-DEC-2000
DEFINITION 261483 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BF443844
VERSION BF443844.1 GI:11503936
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 379)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keefe,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCAGTCACGACG
Plate: 95 row: 0 column: 4
Seq primer: ATTTAGCTGACACTATAG.
FEATURES
source
Location/Qualifiers
1. .379
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 124 a 61 c 69 g 125 t
ORIGIN

Query Match 40.0%; Score 248; DB 10; Length 379;
```

```
Best Local Similarity 89.5%; Pred. No. 2.2e-46;
Matches 290; Conservative 0; Mismatches 30; Indels 4; Gaps 2;

Qy 154 ggaactcaagattgaattcttgaggagaatggcttccattcattcattgagtcgattc 213
|||||
Db 57 GGAACCTTCAAGGTATTAAATCTTAGA-GAATGGCTTTATTTCATGTGAATATCAGATGT 115
|||||
Qy 214 ctctataacctgctgtgttggtgacagcatttggctcta---tgctttcaaatgctgagata 270
|||||
Db 116 CTATATACTCTCTTATTATTGGCACAGCATTTGGCTCTACTTTGCTCTTCAAAATGCCGAGATA 175
|||||
Qy 271 aaagttaactcctcctcaggattttgagatagtggaacctggatattttaggttatctctc 330
|||||
Db 176 AAAGTTAATCTCTCCCAAGATTTTGAATATAGTGGACCTGGATATTTAGGTATCTCTAT 235
|||||
Qy 331 ttgcaatggcaacctccattatttcccggaataattttaaaggaaatgcacaaatgataa 390
|||||
Db 236 TTGCAGTGGCAACCTCCACTGCTCTGGATAAATTTAAGGAATGCACAGTAGATATGAA 295
|||||
Qy 391 ttaataaccgaaacattgatagtgaaactggaagaccattaccagaatctacat 450
|||||
Db 296 TTAATAATACCGAAACATTGATAGTGAAGCTGGAAGACGATCATTTACTTAAGAATCTACAT 355
|||||
Qy 451 taaaaagatgggtttgatctttaac 474
|||||
Db 356 TACAAAGATGGTTTGATCTTAAC 379
|||||

RESULT 8
LOCUS R52795 473 bp mRNA linear EST 18-MAY-1995
DEFINITION y999f10.r1 Soares infant brain lN1B Homo sapiens cDNA clone
IMAGE:41648 5', mRNA sequence.
ACCESSION R52795
VERSION R52795.1 GI:814697
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 473)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissole,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1454
High quality sequence stops: 372
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1454 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 372.
FEATURES
source
Location/Qualifiers
1. .473
/organism="Homo sapiens"
/db_xref="GDB:414189"
/db_xref="taxon:9606"
/clone="IMAGE:41648"
/clone_lib="Soares infant brain lN1B"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
```


for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 210 a 375 c 145 g 174 t
ORIGIN

Query Match 30.4%; Score 188.2; DB 10; Length 904;
Best Local Similarity 77.9%; Pred. No. 9.4e-33;
Matches 306; Conservative 0; Mismatches 73; Indels 14; Gaps 6;

Qy 150 gagtggaaactcaaaagttaaatcttggagggaatgagcttcttcatttcatttggatgtcg 209
Db 27 GAGAGGCAATATCAAGGTTTAAATCTCGAGAAATGGCTTTCGTTTGGCTATCGG 86

Qy 210 attctctatccctgctgtttcacagcatttggct---ctatgctttcaaatgcgga 266
Db 87 ATGCTTATATACCTTCGTGAAGCAACCAATTTGGCTGTACTTTCATCTTCAGACCCGA 146

Qy 267 gataaaagttaatcctctcaggttttgagatagtggaacctggtatattagggttatct 326
Db 147 GATAAAAGCTTAACCTCTCCTCAGGATTTTGAGATAGTGATCCCGGATACTTATAGGTTATCT 206

Qy 327 ctctttgcaatgggaacctccattatttcggataa---ttttaagaatgcacaatag-- 382
Db 207 CTATTTGCAATGGCAACCCCACTGCTCTGTGATCATCTTTAAACGGAAATGCACAGTGCA 266

Qy 383 aatatgaattaaataccgaacatttgata---gtgaaactggaagaccattaccac 439
Db 267 CATATGAACCTAAATACCGAACAATTTGTAGTGGAACACATGGCGCAAGACCATCATCTA 326

Qy 440 agaattcattacaaagtgggttgatctttaacaaagg---tattgaagcaaatgaa 496
Db 327 AGAATCTACATTACAAAGATGGTTTGATCTTAACAAAGGCACCTCTGAACGCGAAGATAC 386

Qy 497 acac-actctgcgcagcaaatgcacaaatgga 528
Db 387 ACAGCGCTTTTACCATGGCAATGCACAAATGGA 419

RESULT 11
BE788633
LOCUS 601475992F1 NIH_MGC_68 715 bp mRNA linear EST 20-OCT-2000
DEFINITION 601475992F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878831 5',
mRNA sequence.
BE788633
VERSION BE788633.1 GI:10209831
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 715)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rcgaps-r@mail.nih.gov
Tissue Procurement: DCTD/BTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9643 row: g column: 24
High quality sequence stop: 575.
Location/Qualifiers
1..715
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3878831"

FEATURES
source

/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SpORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

BASE COUNT 229 a 154 c 141 g 191 t
ORIGIN

Query Match 23.0%; Score 142.4; DB 10; Length 715;
Best Local Similarity 81.6%; Pred. No. 2.4e-22;
Matches 191; Conservative 0; Mismatches 36; Indels 7; Gaps 2;

Qy 394 aaataccgaacatgatgtgaaactggaagaccattaccacgaatctacatc 453
Db 5 AAATACCCGAACATTTGGTAGTGAACATGGGAAGACCATCATTTACTAGAAATCTAGATTAC 64

Qy 454 aaagatgggttgatctttaacaaaggattgaagcaaaagataaacacacctctgccc---a 510
Db 65 AAAGATGGGTTTGATCTTTAACAAGGCGCATTTGAAGCGAAGATACACACGCTTTTACCTAT 124

Qy 511 gcacaatgcacaaatggatca---gaagttagaagttcatggcgagaaactactattg 566
Db 125 CGCCAATGGCAAAACTGGCATACGCAAGTTCAAAGTTCTCTGGCAGAACTACTTATTG 184

Qy 567 gacatccacacaaagaaatcggaactaaatcaaatcaagatatggactgtgata 620
Db 185 GATATCACCAACAGGAATTCAGAAACTAAAGTTTCAGGATATGGATTGGGTATA 238

RESULT 12
BE619361
LOCUS 601473366F1 NIH_MGC_68 755 bp mRNA linear EST 20-OCT-2000
DEFINITION 601473366F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876064 5',
mRNA sequence.
BE619361
VERSION BE619361.1 GI:9890299
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1. (bases 1 to 755)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: rcgaps-r@mail.nih.gov
Tissue Procurement: DCTD/BTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9636 row: d column: 17
High quality sequence stop: 685.
Location/Qualifiers
1..755
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3876064"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SpORT6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

FEATURES
source

BASE COUNT 228 a 131 c 177 g 219 t
ORIGIN

```

Query Match      18.8%; Score 116.6; DB 10; Length 755;
Best Local Similarity 74.08%; Pred. No. 1.8e-16;
Matches 270; Conservative 0; Mismatches 79; Indels 16; Gaps 9;

Qy 161 tcaagattgaattcgtgaggaatggcttcattcatttggatgctgattccctctata 220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 TCAAGGTTTAAATCTCGAGAAAGGGCTTTCGTT-GCTTGGTAATCGGATCTTATATA 61

Qy 221 cctgctctgtttgcacagcatt---tgctctatgctttcattcattcagataaaagtta 277
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 CTTTCTTGATAGACACAACTGGCTGCTACTTCACTTTACAGACACCCAGATATAAAGTGA 121

Qy 278 atcctccctcagattttgagatagc-gaacctctgagattttaggttatct--ctctttgc 334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 ACCCTCCCTCAGATTTTGAGATAGTAGGATCCGGATCTTAGGTATCTCGGTATTTGC 181

Qy 335 aatggcaacccctccatttttcc---ggataattttaagggaatgc--acaatagaaatg 388
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 AATGCCAACCCCGCCACTGTCCTCTGGATCAGTTTAAAGGAATGCTAGCAGTGGAAATG 241

Qy 389 aa-ttaaataccgaaacattgatgtaaaactggaagaccatc-attacaagaatct 446
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 242 AACATAAAATACCGAAACATGCTAGTAAACTATATGGAAGACCATCTATTACTAAGAATCT 301

Qy 447 acattac-aagatgggtttgatcttaaaaggtattgaagcaagataaacacacttc 505
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 AGATTACCGAAGATGGTTGGATCTTAACAGGGCATAGACGGAAGATACACAGCCTTT 361

Qy 506 tgcga 510
    |||
Db 362 GACCA 366

RESULT 13
CNS018GS/c
LOCUS      942 bp      DNA      linear      GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN13p09 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  ALI09318.1 GI:5629622
VERSION     1
KEYWORDS    fruit fly.
SOURCE      Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 942)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (BDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBelOAC11.
FEATURES     Location/Qualifiers
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                        /plasmid="pBelOAC11"
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Query Match      7.3%; Score 45.4; DB 12; Length 1101;
Best Local Similarity 19.3%; Pred. No. 2.8; Mismatches 227; Indels 0; Gaps 0;
Matches 98; Conservative 184; Mismatches 184; Mismatches 227; Indels 0; Gaps 0;

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Qy 528 atcagaagttagaagt 543
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RESULT 14
CNS0039G
LOCUS      1101 bp      DNA      linear      GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION  AL063921
VERSION     1
KEYWORDS    fruit fly.
SOURCE      Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1101)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES     Location/Qualifiers
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                        /note="end : TET3"
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Query Match      7.3%; Score 45.4; DB 12; Length 1101;
Best Local Similarity 19.3%; Pred. No. 2.8; Mismatches 227; Indels 0; Gaps 0;
Matches 98; Conservative 184; Mismatches 227; Indels 0; Gaps 0;

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[illegible]

RESULT 15

AA298563	365 bp	mRNA	linear	EST 18-APR-1997
EST14178	HSC172 cells I	Homo sapiens cDNA	5' end similar to IL13 receptor (IL13R), mRNA sequence.	
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AA298563.1	GI:1950896			
EST.				
human.				
Human sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1 (bases 1 to 365)				
Adams,M.D., Kervilave,A.R., Fleischmann,R.D., Fuldner,R.A., Bult				
,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White				
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,				
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald				
,L.M., Fitzhugh,W.M., Frithman,J.D., Geoghagen,N.S., Glodok,A.,				
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkie,P.S., Jr., Kelley,J.M.,				
Kerley,J.C., Liu,L.-I., Marnaros,S.M., Merrick,J.M.,				
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,				
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley R.,				
Small,K.V., Springs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,				
Bednark,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,				
Dinke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.L.,				
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,				
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,				
Weiy.Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Pannon				
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and				
Venter,J.C.				
Initial assessment of human gene diversity and expression patterns				
based upon 83 million nucleotides of cDNA sequence				
Nature 377 (6547 Suppl), 3-174 (1995)				
96026280				
Other_ESTS: THCl94124				
Contact: Kerlavage, AR				
JOURNAL MEDLINE COMMENT				
TITLE				
JOURNAL MEDLINE COMMENT				

Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tcdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
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ORIGIN

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Best Local Similarity	86.2%	Pred. No. 2.8;		
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Job time: 9700 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 11:31:42 ; Search time 108.29 Seconds
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1406.342 Million cell updates/sec

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Perfect score: 620
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	341.2	55.0	1369	1 US-08-609-572-3	Sequence 3, Appli
2	341.2	55.0	1369	4 US-08-841-751-3	Sequence 3, Appli
3	341.2	55.0	1369	4 US-08-846-340-3	Sequence 3, Appli
4	341.2	55.0	1369	4 US-08-846-344-3	Sequence 3, Appli
5	311.2	50.2	1525	1 US-08-609-572-1	Sequence 1, Appli
6	311.2	50.2	1525	4 US-08-841-751-1	Sequence 1, Appli
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11	35.2	5.7	4797	4 US-09-354-243B-25	Sequence 25, Appli
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16	33.8	5.5	1991	4 US-08-235-836C-77	Sequence 77, Appli
c 17	33.8	5.5	43795	3 US-08-742-185-101	Sequence 101, App
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19	33.4	5.4	9636	1 US-08-323-170B-1	Sequence 1, Appli
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Sequence 108, App
Sequence 108, App
Sequence 16, Appl
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Sequence 18, Appl
Sequence 101, App
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Sequence 21, Appl
Sequence 21, Appl
Sequence 22, App
Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-08-609-572-3
; Sequence 3, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whittiers, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
US-08-609-572-3

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Sequence 16, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 18, Appl
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Sequence 21, Appl
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Sequence 75, Appl

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Query Match 55.0%; Score 341.2; DB 1; Length 1369;
Best Local Similarity 84.0%; Pred. No. 2.6e-85;
Matches 398; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

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RESULT 2
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; Sequence 3, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A. 32,724
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: G15268
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TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
; US-08-841-751-3

Query Match 55.0%; Score 341.2; DB 4; Length 1369;
Best Local Similarity 84.0%; Pred. No. 2.6e-85;
Matches 398; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 150 gagtggaacttcaaaagtattgaatctctggagggaatggctttcatttcatttggatgctgg 209
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Db 489 GATATCACCACACAGGAATTCAGAAACTTAAAGTTTCAGGATATGGATTCGGTATA 542

RESULT 3
US-08-846-340-3
; Sequence 3, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
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Qy 447 acattacaaagctgggtttgattcttaacaaaggtattgaagcaaaagataaacaactct 506
Db 369 AATTACAAAGATGGTTTGATCTTTAACAGGGCATTTGAAGCGAAGATACACACGCTTTT 428
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RESULT 5

US-08-609-572-1
; Sequence 1, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
US-08-609-572-1

Query Match 50.2%; Score 311.2; DB 1; Length 1525;
Best Local Similarity 74.8%; Pred. No. 5.3e-77;
Matches 437; Conservative 0; Mismatches 128; Indels 19; Gaps 3;
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Qy 97 aggacctgtgaattgcctatgataaattcattctttttgagaacacattattattgagtga 156
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Qy 217 tataccctgcttggttgacagcatttggctctctatgctttccaaatgctgagataaaaaagt 276
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Db 634 GAAGGAAGTTGGAAACTAAAAATTCAGGACATGAAGTGTATATA 677

RESULT 6

US-08-841-751-1
; Sequence 1, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1404
US-08-841-751-1

Query Match 50.2%; Score 311.2; DB 4; Length 1525;
Best Local Similarity 74.8%; Pred. No. 5.3e-77;
Matches 437; Conservative 0; Mismatches 128; Indels 19; Gaps 3;
Qy 37 aggaaggagcttagagattcctaattgctctccaaactggagagagagagagagagagag 96
Db 113 AGGAAGGAAACAGTAGAGATTCAATTTAGTGTCT- - - - AATGTGGAAGGAGGACAAAG 168
Qy 97 aggaacctgataatgcctatgataattcatttcttgagaaaccattattttagtgga 156
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Db 634 GAAGGAAGTTTGGAAACTTAAATTCAGGACATGAAGTGTATATA 677

RESULT 7
US-08-846-340-1
Sequence 1, Application US/08846340
Patent No. 6248714
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive

TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,340
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1404
US-08-846-340-1

Query Match 50.2%; Score 311.2; DB 4; Length 1525;
Best Local Similarity 74.8%; Pred. No. 5.3e-77;
Matches 437; Conservative 0; Mismatches 128; Indels 19; Gaps 3;
Qy 37 aggaaggagcttagagattcctaattgctctccaaactggagagagagagagagagagag 96
Db 113 AGGAAGGAAACAGTAGAGATTCAATTTAGTGTCT- - - - AATGTGGAAGGAGGACAAAG 168
Qy 97 aggaacctgataatgcctatgataattcatttcttgagaaaccattattttagtgga 156
Db 169 AGGCTCTGTGATACTGCTGTGATAATACATTTCTTGAGAAACCATTATTATTGAGTAGA 228
Qy 157 aacttcaagattgaaactctggaggaatggcttctcatttggatgcggattcctc 216
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QY 577 caagaaatcggaactaaattcaagatatggactgtgata 620
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Db 634 GAAGGAAGTTTGGAAACTAAAATTCCAGGACATGAAGTGTATATA 677
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RESULT 8
US-08-846-344-1
; Sequence 1, Application US/08846344
; Patent No. 6268480
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,344
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
; US-08-846-344-1

Query Match 50.2%; Score 311.2; DB 4; Length 1525;
Best Local Similarity 74.8%; Pred. No. 5.3e-77;
Matches 437; Conservative 0; Mismatches 128; Indels 19; Gaps 3;
QY 37 eaggagggaagctcttagagattcttaataatgtctccaaactggagagagaaaaaaag 96
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RESULT 9
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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
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RESULT 14
US-08-559-896B-1
; Sequence 1, Application US/08559896B
; Patent No. 6310046
; GENERAL INFORMATION:
; APPLICANT: Patrick E. Duffy
; APPLICANT: Christian F. Ockenhouse
; TITLE OF INVENTION: SEQUESTRAIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: USA NPMC MCMR-JA
; CITY: FORT DETRICK, FREDERICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,896B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1956 base pairs
; TYPE: Nucleic acid

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

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(without alignments)
1903.657 Million cell updates/sec

Title: US-09-828-995b-54

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	620	100.0	1454	22	Canine interleukin
5	437	70.5	1158	22	Canine interleukin
6	437	70.5	1158	22	Canine interleukin
7	374	60.3	954	22	Canine IL-13R extr
8	374	60.3	954	22	Canine IL-13R extr
9	374	60.3	1095	22	Canine interleukin

c	10	374	60.3	1095	22	AAS59967	Canine interleukin
c	11	374	60.3	1686	22	AAS59970	Canine IL-13R/IgG-
c	12	374	60.3	1686	22	AAS59971	Canine IL-13Ralpha
c	13	374	60.3	1686	22	AAS59976	Canine IL-13R/IgG-
c	14	374	60.3	1686	22	AAS59977	Canine IL-13Ralpha
c	15	374	60.3	1692	22	AAS59974	Canine IL-13R/IgG-
c	16	374	60.3	1692	22	AAS59975	Canine IL-13Ralpha
c	17	374	60.3	1698	22	AAS59972	Canine IL-13R/IgG-
c	18	374	60.3	1698	22	AAS59973	Canine IL-13Ralpha
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c	20	341.2	55.0	1298	18	AAT86464	Human interleukin-
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c	23	341.2	55.0	1369	21	AAA27912	Human interleukin-
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c	29	338.8	54.6	1288	19	AAV04075	Human cytokine/pep
c	30	338.8	54.6	1288	19	AAV02295	Homo sapiens cDNA
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ALIGNMENTS

RESULT 1

AAS59958

ID AAS59958 standard; cDNA; 620 BP.

XX AC AAS59958;

XX DT 29-JAN-2002 (first entry)

XX DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 620.

XX DE Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;

KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG FC;

KW Immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;

KW Immune response.

XX OS Canis familiaris.

XX OS Canis familiaris.

XX PN WO200177332-A2.

XX XX 18-OCT-2001.

XX PF 09-APR-2001; 2001WO-US11498.

XX PR 07-APR-2000; 2000US-195659P.

XX PR 07-APR-2000; 2000US-195874P.

XX PA (HESK-) HESKA CORP.

XX PI McCall CA, Tang L;

XX XX WPI; 2001-657172/75.

DR P-PSDB; AAU69133.

Db 440 GGAATGGCTTCATTCATTTGGATGTCGGATTCCTCTATACCCCTGCTGTTTGACAGCA 381
Qy 241 ttggctctatgctttcaaatgctgagataaaagtttaactctctcaggaatttgagata 300
Db 380 TTTGGCTCTATGCTTCAATGCTGAGATAAAAGTTAATCTCTCAGGATTTTGAGATA 321
Qy 301 gtggacctggatattaggtatctctctcttgcgaatggcaacctcaattttccggat 360
Db 320 GTGACCTGGATATTTAGGTTATCTCTCTTTGCAATGGCAACCTCCATTTATTTCCGGAT 261
Qy 361 aatttaagaaatgcacaatagaatgaattaaataaccgaacattgatagtaaac 420
Db 260 AATTTAAGGAATGCACAATAGAAATATGAATTAATAATACCGAAACATGTGATGGAAC 201
Qy 421 tggagaccatcattaccagaatctacattacaagaatgggttgatcttaacaaagt 480
Db 200 TGGAGACCATCATACCAAGAACTACATTACAAGATGGTTGATCTTAACAAAGGT 141
Qy 481 attgaagcaagaataaacacactctctgcagcacaatgcacaaatgatcagaagttaga 540
Db 140 ATTGAAGCAAGATAAACACACTTCTGCCAGCACAAATGCACAAATGGATCAGAAAGTTAGA 81
Qy 541 agttcatgggcagaaactactatttgacatcaccaagaagaaatcggaactaaaatt 600
Db 80 AGTTATGGGCAGAACTACTTATTGGACATCACCAAGGAATCGGAAACTAAAAATT 21
Qy 601 caagatatgactgtgtata 620
Db 20 CAAGATATGGACTGTGTATA 1
RESULT 3
AAS59962
ID AAS59962 standard; cDNA; 1454 BP.
XX AC AAS59962;
XX DT 29-JAN-2002 (first entry)
XX DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1454.
XX KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
XX KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX KW immune response.
XX OS Canis familiaris.
XX OS WO200177332-A2.
XX PN 18-OCT-2001.
XX PD 09-APR-2001; 2001WO-US11498.
XX PF 07-APR-2000; 2000US-195659P.
XX PR 07-APR-2000; 2000US-195874P.
XX PR (HESK-) HESKA CORP.
XX PA
XX PI McCall CA, Tang L;
XX PI WPI; 2001-657172/75.
XX DR P-PSDB; AAU69135.
XX DR
XX PT Novel isolated canine protein, preferably canine immunoglobulin G
XX PT protein or canine interleukin-13 receptor protein useful for regulating
XX PT immune response of an animal and for developing regulatory compounds
XX PS Claim 19; Page 173-175; 22lpp; English.
XX CC The invention concerns an isolated canine protein, preferably canine
XX CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)

CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for developing an immune response in a canine. The proteins are useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
SQ Sequence 1454 BP; 491 A; 238 C; 282 G; 442 T; 1 other;
Query Match 100.0%; Score 620; DB 22; Length 1454;
Best Local Similarity 100.0%; Pred. No. 1.4e-153;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ggcacgaggctgagtttgcttgattatcagacaggaagggaagctcttagagattct 60
Db 1 ggcacgaggctgagtttgcttgattatcagacaggaagggaagctcttagagattct 60
Qy 61 aatttaagtctccaaactggagagagaaaaaaggagacctgtgataattgacctatga 120
Db 61 aatttaagtctccaaactggagagagaaaaaaggagacctgtgataattgacctatga 120
Qy 121 taattcattcttgagaaacattatttgatgagtgaaacttcaagtattgaactctgga 180
Db 121 taattcattcttgagaaacattatttgatgagtgaaacttcaagtattgaactctgga 180
Qy 181 ggaatggcttcatttcatttgatgctggatctctctataccctgctgtttgcacagca 240
Db 181 ggaatggcttcatttcatttgatgctggatctctctataccctgctgtttgcacagca 240
Qy 241 ttggctctatgctttcaaatgctgagataaaagttaactctctcaggaatttgagata 300
Db 241 ttggctctatgctttcaaatgctgagataaaagttaactctctcaggaatttgagata 300
Qy 301 gtgaccttgatattaggttatctctcttgcgaatggcaacctccattttccggat 360
Db 301 gtgaccttgatattaggttatctctcttgcgaatggcaacctccattttccggat 360
Qy 361 aattttaagggaatgcacaatagaatgaattaaataaccgaacattgatagtaaac 420
Db 361 aattttaagggaatgcacaatagaatgaattaaataaccgaacattgatagtaaac 420
Qy 421 tggagaccatcattaccagaatctacattacaagaatgggtttgatcttaacaaagt 480
Db 421 tggagaccatcattaccagaatctacattacaagaatgggtttgatcttaacaaagt 480
Qy 481 attgaagcaagaataaacacacttctccagcacaatgcacaaatggatcagaagttaga 540
Db 481 attgaagcaagaataaacacacttctccagcacaatgcacaaatggatcagaagttaga 540
Qy 541 agttcatgggcagaaactactatttgacatcaccaagaagaaatcgggaaactaaaatt 600
Db 541 agttcatgggcagaaactactatttgacatcaccaagaagaaatcgggaaactaaaatt 600
Qy 601 caagatatggactgtgtata 620
Db 601 caagatatggactgtgtata 620
RESULT 4
AAS59963/c
ID AAS59963 standard; cDNA; 1454 BP.
XX AC AAS59963;
XX DT 29-JAN-2002 (first entry)
XX DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1454 complement.

CC therapy). The present sequence encodes a protein of the invention.

XX
SQ Sequence 1158 BP; 380 A; 201 C; 224 G; 353 T; 0 other;

Query Match 70.5%; Score 437; DB 22; Length 1158;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 atggcttcattcattgagatgcgattcctctctataccctgctgttgcacagcattt 243
Db 1 atggcttcattcattgagatgcgattcctctctataccctgctgttgcacagcattt 60
Qy 244 ggctctatgcttcaaaatgcgtgagataaaagttaactcctcctcaggtttgagatagtg 303
Db 61 ggctctatgcttcaaaatgcgtgagataaaagttaactcctcctcaggtttgagatagtg 120
Qy 304 gacctgcatattaggttatctctcttgcgaatgcgaacctccattttccggataat 363
Db 121 gacctgcatattaggttatctctcttgcgaatgcgaacctccattttccggataat 180
Qy 364 tttaagggaatgcacaaatgaatgaattaaataaccgaaacattgtagtgaactgg 423
Db 181 tttaagggaatgcacaaatgaatgaattaaataaccgaaacattgtagtgaactgg 240
Qy 424 aagaccattaccacaaatgcattacattacaaagatgggtttgatcttaacaaaagtatt 483
Db 241 aagaccattaccacaaatgcattacattacaaagatgggtttgatcttaacaaaagtatt 300
Qy 484 gaagcaagataaaacacactcttcgcagcaacaatgcacaaatggatcagaagttagaagt 543
Db 301 gaagcaagataaaacacactcttcgcagcaacaatgcacaaatggatcagaagttagaagt 360
Qy 544 tcattgggcagaaactactatttgacatcacacagaagaatcgggaaactaaattcaa 603
Db 361 tcattgggcagaaactactatttgacatcacacagaagaatcgggaaactaaattcaa 420
Qy 604 gatatggactgtgtata 620
Db 421 gatatggactgtgtata 437

RESULT 6
AAS59965/c
ID AAS59965 standard; cDNA; 1158 BP.
XX
AC AAS59965;
XX
DT 29-JAN-2002 (first entry)
XX
XX Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1158 complement.
DE
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
XX 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
XX (HESK*) HESKA CORP.
XX
XX McCall CA, Tang L;
PI
XX
DR WPI; 2001-657172/75.

XX
PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Claim 19; Page 179; 221pp; English.
PS
XX The invention concerns an isolated canine protein, preferably canine
XX immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins are useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX
SQ Sequence 1158 BP; 353 A; 224 C; 201 G; 380 T; 0 other;

Query Match 70.5%; Score 437; DB 22; Length 1158;
Best Local Similarity 100.0%; Pred. No. 2.1e-105;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 atggcttcattcattgagatgcgattcctctctataccctgctgttgcacagcattt 243
Db 1158 atggcttcattcattgagatgcgattcctctctataccctgctgttgcacagcattt 1099
Qy 244 ggctctatgcttcaaaatgcgtgagataaaagttaactcctcctcaggtttgagatagtg 303
Db 1098 ggctctatgcttcaaaatgcgtgagataaaagttaactcctcctcaggtttgagatagtg 1039
Qy 304 gacctgcatattaggttatctctcttgcgaatgcgaacctccattttccggataat 363
Db 1038 gacctgcatattaggttatctctcttgcgaatgcgaacctccattttccggataat 979
Qy 364 tttaagggaatgcacaaatgaatgaattaaataaccgaaacattgtagtgaactgg 423
Db 978 tttaagggaatgcacaaatgaatgaattaaataaccgaaacattgtagtgaactgg 919
Qy 424 aagaccattaccacaaatgcattacattacaaagatgggtttgatcttaacaaaagtatt 483
Db 918 aagaccattaccacaaatgcattacattacaaagatgggtttgatcttaacaaaagtatt 859
Qy 484 gaagcaagataaaacacactcttcgcagcaacaatgcacaaatggatcagaagttagaagt 543
Db 858 gaagcaagataaaacacactcttcgcagcaacaatgcacaaatggatcagaagttagaagt 799
Qy 544 tcattgggcagaaactactatttgacatcacacagaagaatcgggaaactaaattcaa 603
Db 798 tcattgggcagaaactactatttgacatcacacagaagaatcgggaaactaaattcaa 739
Qy 604 gatatggactgtgtata 620
Db 738 gatatggactgtgtata 722

RESULT 7
AAS59968
ID AAS59968 standard; cDNA; 954 BP.
XX
AC AAS59968;
XX
XX 29-JAN-2002 (first entry)
XX
XX Canine IL-13R extracellular domain cDNA nCaIL-13Ralpha2 954.
DE
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW

KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.

XX Canis familiaris.

XX WO200177332-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-US11498.

XX 07-APR-2000; 2000US-195659P.

XX 07-APR-2000; 2000US-195874P.

XX (HESK-) HESKA CORP.

XX McCall CA, Tang L;

XX WPI; 2001-657172/75.

XX P-PSDB; AAU69137.

XX Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -

XX Claim 19; Page 184-185; 221pp; English.

XX The invention concerns an isolated canine protein, preferably canine
 CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, fusion proteins between the IgG and IL-13R proteins
 CC and methods of isolating regulators of them. The regulators are useful
 CC for regulating an immune response in a canine. The proteins are useful to
 CC develop regulatory compounds including inhibitors and activators that,
 CC when administered to a canine in an effective manner, are capable of
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene
 CC therapy). The present sequence encodes a protein of the invention.

XX Sequence 954 BP; 329 A; 162 C; 192 G; 271 T; 0 other;

Query Match 60.3%; Score 374; DB 22; Length 954;

Best Local Similarity 100.0%; Pred. No. 7.7e-89;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 tctatgctttcaaatgctgagataaaagttaattctctcctcaggattttgagataggac 306

DB 4 tctatgctttcaaatgctgagataaaagttaattctctcctcaggattttgagataggac 63

QY 307 cctgatatattaggattatctctcttgcaatggcaacctccattatttccggataatttt 366

DB 64 cctgatatattaggattatctctcttgcaatggcaacctccattatttccggataatttt 123

QY 367 aaggatgcacatagaatatgaattaaataaccgaacattgtagtgaacactggaag 426

DB 124 aaggatgcacatagaatatgaattaaataaccgaacattgtagtgaacactggaag 183

QY 427 accatcattaccagaatctacattacaaagatgggtttgtattcttaacaaaggattgaa 486

DB 184 accatcattaccagaatctacattacaaagatgggtttgtattcttaacaaaggattgaa 243

QY 487 gcaagataaaacacactctgcagacacaaatgcacaaatggatcagaagttgaagtcca 546

DB 244 gcaagataaaacacactctgcagacacaaatgcacaaatggatcagaagttgaagtcca 303

QY 547 tgggcagaaactactatttggacatcaccacagaagaatcgggaaactaaattcaagat 606

DB 304 tgggcagaaactactatttggacatcaccacagaagaatcgggaaactaaattcaagat 363

QY 607 atggactgtgtata 620

DB 364 atggactgtgtata 377

RESULT 8

AAS59969/c

XX AAS59969 standard; cDNA; 954 BP.

XX AAS59969;

XX 29-JAN-2002 (first entry)

XX Canine IL-13R extracellular domain cDNA nCaIL-13Ralpha2 954 complement.

XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;

XX IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;

XX immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;

XX immune response.

XX Canis familiaris.

XX WO200177332-A2.

XX 18-OCT-2001.

XX 09-APR-2001; 2001WO-US11498.

XX 07-APR-2000; 2000US-195659P.

XX 07-APR-2000; 2000US-195874P.

XX (HESK-) HESKA CORP.

XX McCall CA, Tang L;

XX WPI; 2001-657172/75.

XX Novel isolated canine protein, preferably canine immunoglobulin G

PT protein or canine interleukin-13 receptor protein useful for regulating

PT immune response of an animal and for developing regulatory compounds -

XX Claim 19; Page 187; 221pp; English.

XX The invention concerns an isolated canine protein, preferably canine
 CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, fusion proteins between the IgG and IL-13R proteins
 CC and methods of isolating regulators of them. The regulators are useful
 CC for regulating an immune response in a canine. The proteins are useful to
 CC develop regulatory compounds including inhibitors and activators that,
 CC when administered to a canine in an effective manner, are capable of
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene
 CC therapy). The present sequence is the reverse complement of a cDNA
 CC encoding a protein of the invention.

XX Sequence 954 BP; 271 A; 192 C; 162 G; 329 T; 0 other;

Query Match 60.3%; Score 374; DB 22; Length 954;

Best Local Similarity 100.0%; Pred. No. 7.7e-89;

Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 tctatgctttcaaatgctgagataaaagttaattctctcctcaggattttgagataggac 306

DB 951 TCTATGCTTCAAAATGCTGAGATAAAAGTTAAATCTCTCTCAGGATTTTTCAGATAGTGGAC 892

QY 307 cctgatatattaggattatctctcttgcaatggcaacctccattatttccggataatttt 366

DB 891 CCTGATATTTAGTTATCTCTTTGCAATGGCAACCTCCATTATTTCCGGATAATTTT 832

Qy 367 aaggaatgcacaataagaataatgaataataaaataccgaaacattgatagtgaaactgggaag 426
 Db 831 AAGGAATGCACAATAGAATATGAATTAATAATACCGAAACATGTATGATGAACCTGGGAAG 772

Qy 427 accatcattaccagaactctcatcattacaaagatgggtttgatcttaacaaaggtattgaa 486
 Db 771 ACCATCATTACCAGAATCTACATTACAAAGATGGGTTTGATCTTAACAAGGTATTGAA 712

Qy 487 gcaagataaacacacactctccagcacaatgcacaaatggatcgagaagttagaagtcca 546
 Db 711 GCAAGATAAACACACTTCTGCCAGCACAAATGCACAAATGGATCGAAGTTAGAAGTTCA 652

Qy 547 tgggcagaaactactatttgacatcaccacaaagaaatcgggaaactaaattcaaat 606
 Db 651 TGGGCAGAAACTACTATTGTGGACATCACCAAGAAATCGGAAACTAAAAATTCAGAT 592

Qy 607 atggactgtgata 620
 Db 591 ATGGACTGTGTATA 578

RESULT 9
 AAS59966
 ID AAS59966 standard; cdna; 1095 BP.
 XX AC AAS59966;
 XX DT 29-JAN-2002 (first entry)
 XX DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1095.
 XX KW Dog; interleukin-13 receptor alpha; interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.
 XX OS Canis familiaris.
 XX PN WO200177332-A2.
 XX PD 18-OCT-2001.
 XX PF 09-APR-2001; 2001WO-US11498.
 XX PR 07-APR-2000; 2000US-195659P.
 XX PR 07-APR-2000; 2000US-195874P.
 XX PA (HESK-) HESKA CORP.
 XX PI McCall CA, Tang L;
 XX DR WPI; 2001-657172/75.
 XX DR P-PSDB; RAU69136.
 XX PT Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 XX Claim 19; Page 179-181; 221pp; English.

The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13R proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence encodes a protein of the invention.

XX SQ Sequence 1095 BP; 370 A; 186 C; 211 G; 328 T; 0 other;
 Query Match 60.3%; Score 374; DB 22; Length 1095;
 Best Local Similarity 100.0%; Pred. No. 8e-89;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 tctatgcttcaaaatgctgagataaaagttaactctctcctcagcagattttgagatagtgac 306
 Db 1 tctatgcttcaaaatgctgagataaaagttaactctctcctcagcagattttgagatagtgac 60

Qy 307 cctggaatttaggttatctctctcttgcattgcaatggcgaactccattttcccgataatttt 366
 Db 61 cctggaatttaggttatctctctcttgcattgcaatggcgaactccattttcccgataatttt 120

Qy 367 aaggaatgcacaataagaataatgaaataaaatcaccgaacattgatagtgaaactgggaag 426
 Db 121 aaggaatgcacaataagaataatgaaataaaatcaccgaacattgatagtgaaactgggaag 180

Qy 427 accatcattaccagaactctcatcattacaaagatgggtttgatcttaacaaaggtattgaa 486
 Db 181 accatcattaccagaactctcatcattacaaagatgggtttgatcttaacaaaggtattgaa 240

Qy 487 gcaagataaacacacactcttgcagcacaatgcacaaatggatcgagaagttagaagtcca 546
 Db 241 gcaagataaacacacactcttgcagcacaatgcacaaatggatcgagaagttagaagtcca 300

Qy 547 tgggcagaaactactatttgacatcaccacaaagaaatcgggaaactaaattcaaat 606
 Db 301 tgggcagaaactactatttgacatcaccacaaagaaatcgggaaactaaattcaaat 360

Qy 607 atggactgtgata 620
 Db 361 atggactgtgata 374

RESULT 10
 AAS59967/c
 ID AAS59967 standard; cdna; 1095 BP.
 XX AC AAS59967;
 XX DT 29-JAN-2002 (first entry)
 XX DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1095 complement.
 XX KW Dog; interleukin-13 receptor alpha; interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.
 XX OS Canis familiaris.
 XX PN WO200177332-A2.
 XX PD 18-OCT-2001.
 XX PF 09-APR-2001; 2001WO-US11498.
 XX PR 07-APR-2000; 2000US-195659P.
 XX PR 07-APR-2000; 2000US-195874P.
 XX PA (HESK-) HESKA CORP.
 XX PI McCall CA, Tang L;
 XX DR WPI; 2001-657172/75.
 XX PT Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 XX

```
PS Claim 19; Page 183; 221pp; English.
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
XX encoding a protein of the invention.
SQ Sequence 1095 BP; 328 A; 211 C; 186 G; 370 T; 0 other;

Query Match      60.3%; Score 374; DB 22; Length 1095;
Best Local Similarity 100.0%; Pred. No. 8e-89;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 tctatgctttcaaaatgctgagataaaaagttaatcctctcaggattttgagataggac 306
Db 1095 TCTATGCTTTCAAATGCTGAGATAAAAAGTTAATCCTCTCAGGATTTGAGATAGTGGAC 1036

QY 307 cctggatatttaggttatctctcttgaatggaatggaacctccattattccggataatttt 366
Db 1035 CCTGGATATTTAGGTTATCTCTCTTGAATGGCAACCTCCATTATTTCCGGATATTTT 976

QY 367 aaggatgcacaaatagaatgaattaaataaccgaacattgatgtgaaaactggaag 426
Db 975 AAGGAATGCACAAATAGATATGAATAAATACCCGAACATTTGATAGTCAAAACTGGGAAG 916

QY 427 accatcattaccagaatctacattacaaaagatgggtttgatctcttaacaaagttatgaa 486
Db 915 ACCATCATTTACCAAGAATCTACATTACAAAGATGGTTTGATCTTTAAACAAGGTATTGAA 856

QY 487 gcaagataaaacacacctctgcgcagcacaaatgcacaaatggatcagaagttagaagtcca 546
Db 855 GCAAGATAAAACACACACTTCTGCCGACACAATGCACAAATGGATCAGAAGTTAGAAGTTCA 796

QY 547 tgggcagaaactacttattggacatcacacaaaggaaatcgggaaactaaataattcaagat 606
Db 795 TGGGCAGAAACTACTTATTGGACATCACCAACAGGAATCGGGAACATAAAATTCAAGAT 736

QY 607 atggactgtgtata 620
Db 735 ATGGACTGTGTATA 722

RESULT 11
AAS59970
ID AAS59970 standard; cDNA; 1686 BP.
XX AC AAS59970;
XX AC AAS59970;
XX AC AAS59970;
DT 29-JAN-2002 (first entry)
XX DE Canine IL-13R/IgG-Fc fusion protein cDNA nCaIL-13Ralpha2-Fc3523 1683.
XX KW Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW Immunoglobulin light chain; Lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX OS Canis familiaris.
XX PN WO200177332-A2.
XX PD 18-OCT-2001.

XX 09-APR-2001; 2001WO-US11498.
PF 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX (HESK-) HESKA CORP.
PI McCall CA, Tang L;
DR WPI; 2001-657172/75.
DR P-PSDB; AAU69138.
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX Claim 37; Page 187-190; 221pp; English.
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX Sequence 1686 BP; 513 A; 384 C; 382 G; 407 T; 0 other;

Query Match      60.3%; Score 374; DB 22; Length 1686;
Best Local Similarity 100.0%; Pred. No. 9.2e-89;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 tctatgctttcaaaatgctgagataaaaagttaatcctctcaggattttgagataggac 306
Db 4 tctatgctttcaaaatgctgagataaaaagttaatcctctcaggattttgagataggac 63

QY 307 cctggatatttaggttatctctcttgaatggaatggaacctccattattccggataatttt 366
Db 64 cctggatatttaggttatctctcttgaatggaatggaacctccattattccggataatttt 123

QY 367 aaggatgcacaaatagaatgaattaaataaccgaacattgatgtgaaaactggaag 426
Db 124 aaggatgcacaaatagaatgaattaaataaccgaacattgatgtgaaaactggaag 183

QY 427 accatcattaccagaatctacattacaaaagatgggtttgatctcttaacaaagttatgaa 486
Db 184 accatcattaccagaatctacattacaaaagatgggtttgatctcttaacaaagttatgaa 243

QY 487 gcaagataaaacacacctctgcgcagcacaaatgcacaaatggatcagaagttagaagtcca 546
Db 244 gcaagataaaacacacctctgcgcagcacaaatgcacaaatggatcagaagttagaagtcca 303

QY 547 tgggcagaaactacttattggacatcacacaaaggaaatcgggaaactaaataattcaagat 606
Db 304 tgggcagaaactacttattggacatcacacaaaggaaatcgggaaactaaataattcaagat 363

QY 607 atggactgtgtata 620
Db 364 atggactgtgtata 377

RESULT 12
AAS59971/C
ID AAS59971 standard; cDNA; 1686 BP.
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Db      4  tctatgcttcaaaatgctgagataaaagttaatactctctcctcaggattttgagatagtgac 63
Qy      307 cctgatatattagggttatctctcttgcgaatggaacccctccatttcccggaataatttt 366
Db      64  cctgatatattagggttatctctcttgcgaatggaacccctccatttcccggaataatttt 123
Qy      367 aagggaatgcacaataagaatgaataaaataaccgaacacatgtagtgaataactgggaag 426
Db      124 aagggaatgcacaataagaatgaataaaataaccgaacacatgtagtgaataactgggaag 183
Qy      427 accatcattaccagaatctacattacaaagaatgggttgcattcttcaacaaaggattttaa 486
Db      184 accatcattaccagaatctacattacaaagaatgggttgcattcttcaacaaaggattttaa 243
Qy      487 gcaaaagataaaacacactctcgcagcacacaatgcacaaatggaatggaatggaatttca 546
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Qy      547 tgggcagaaactactatttggacatcacacacaggaataatcggaataactaaattcaagat 606
Db      304 tgggcagaaactactatttggacatcacacacaggaataatcggaataactaaattcaagat 363
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Db      364 atggactgtgtata 377

RESULT 14
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ID      AAS59977 standard; cDNA; 1686 BP.
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AC      AAS59977;
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DT      29-JAN-2002 (first entry)
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DE      Canine IL-13Ralpha2/IgG-Fc fusion protein cDNA reverse complement #4.
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KW      Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW      IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
KW      immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW      immune response.
XX
OS      Canis familiaris.
XX
PN      WO200177332-A2.
XX
PD      18-OCT-2001.
XX
PF      09-APR-2001; 2001WO-US11498.
XX
PR      07-APR-2000; 2000US-195659P.
PR      07-APR-2000; 2000US-195874P.
XX
PA      (HESK-) HESKA CORP.
XX
PI      McCall CA, Tang L;
XX
DR      WPI; 2001-657172/75.
XX
PT      Novel isolated canine protein, preferably canine immunoglobulin G
PT      protein or canine interleukin-13 receptor protein useful for regulating
PT      immune response of an animal and for developing regulatory compounds -
XX
PS      Claim 37; Page 212-213; 221pp; English.
XX
CC      The invention concerns an isolated canine protein, preferably canine
CC      immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC      receptor protein, the nucleic acids encoding them, antibodies
CC      raised against them, fusion proteins between the IgG and IL-13 proteins
CC      and methods of isolating regulators of them. The regulators are useful
CC      for regulating an immune response in a canine. The proteins useful to
CC      develop regulatory compounds including inhibitors and activators that,
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CC      when administered to a canine in an effective manner, are capable of
CC      protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC      regulators are useful for treating canine IgG (heavy and/or light chain)
CC      and/or canine IL-13R mediated responses. The molecules of the invention
CC      are useful to regulate the immune response of an animal (e.g. by gene
CC      therapy). The present sequence is the reverse complement of a cDNA
CC      encoding a protein of the invention.
XX
SQ      Sequence 1686 BP; 407 A; 379 C; 388 G; 512 T; 0 other;

Query Match      60.3%; Score 374; DB 22; Length 1686;
Best Local Similarity 100.0%; Pred. No. 9.2e-89;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      427  accatcattaccagaatctacattacaaagaatgggttgcattcttcaacaaaggattttaa 486
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Qy      487  gcaaaagataaaacacactctcgcagcacacaatgcacaaatggaatggaatggaatttca 546
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Db      1323  atggactgtgtata 1310

RESULT 15
AAS59974
ID      AAS59974 standard; cDNA; 1692 BP.
XX
AC      AAS59974;
XX
DT      29-JAN-2002 (first entry)
XX
DE      Canine IL-13R/IgG-Fc fusion protein cDNA nCaIl-13Ralpha2-Fc-B9 1689.
XX
KW      Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW      IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
KW      immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW      immune response.
XX
OS      Canis familiaris.
XX
PN      WO200177332-A2.
XX
PD      18-OCT-2001.
XX
PF      09-APR-2001; 2001WO-US11498.
XX
PR      07-APR-2000; 2000US-195659P.
PR      07-APR-2000; 2000US-195874P.
XX
PA      (HESK-) HESKA CORP.
XX
PI      McCall CA, Tang L;
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XX WPI; 2001-657172/75.
DR P-PSDB: AAU69140.
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Claim 37; Page 200-203; 221pp; English.
XX
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13alpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
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XX Sequence 1692 BP; 518 A; 376 C; 385 G; 413 T; 0 other;
SQ

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Query Match 60.3%; Score 374; DB 22; Length 1692;
 Best Local Similarity 100.0%; Pred. No. 9.3e-89;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 307 cctggataattaggttattctctcttgcattggcaacctccattatttccggataatttt 366
Db 64 cctggataattaggttattctctcttgcattggcaacctccattatttccggataatttt 123
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Db 124 aaggaatgcacaatagatatgaattaaataccgaaacattgatagtgaactgggaag 183
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Db 184 accatcattacaagaattcattacaaagatgggtttgatcttaacaaaggatttgaa 243
Qy 487 gcaaaagataaacacacttctgccagcacaaatgcacaaatgatcagaagttagaagtcca 546
Db 244 gcaaaagataaacacacttctgccagcacaaatgcacaaatgatcagaagttagaagtcca 303
Qy 547 tgggcagaaactacttattgacatccacacaaagaaatcggaactaaaattcaagat 606
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Qy 607 atggactgtgtata 620
Db 364 atggactgtgtata 377

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 Job time: 17338 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 11:31:47 ; Search time 5720.3 Seconds
(without alignments)
2268.142 Million cell updates/sec

Title: US-09-828-995B-54

Perfect score: 620

Sequence: 1 ggcacgagcgtgagttgtg.....caagatatggactgtgtata 620

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: gb_in.*

4: gb_om.*

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6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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ALIGNMENTS

RESULT 1

AX280319

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Source

CDS

linear PAT 02-NOV-2001

DNA

620 bp

Sequence 54 from Patent WO0177332.

AX280319

AX280319

AX280319.1

GI:16607697

dog.

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (sites)

McCall, C.A. and Tang, L.

Compositions and methods related to canine igg and canine il-13

receptors

Patent: WO 0177332-A 54 18-OCT-2001;

Heska Corporation (US)

Location/Qualifiers

1..620

/organism="Canis familiaris"

/db_xref="taxon:9615"

184..>618

/note="unnamed protein product"

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BASE COUNT 212 a 102 c 127 g 179 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2e-127;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 aattaatgtctccaaactggagaagaaaaaaagagacctgtgataattgcctatga 120
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Qy 121 taattcattcttggagaaccatattattgagtggaacctcaaaagcttgaattcttga 180
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Qy 181 ggaatggcttctcattcatttgatctcgattccctctatcacctctgttggcacagca 240
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Qy 301 gtggacctggattattaggttatctctcttggcaatggcaacctccattttccggat 360
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Qy 361 aatttaagggaatgcacataagaaatgaaattaaataaccgaacattgatgaaac 420
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RESULT 2
AX280321/c
LOCUS Sequence 56 from Patent WO0177332.
DEFINITION AX280321
ACCESSION AX280321
VERSION AX280321.1 GI:16607699
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13

receptors
Patent: WO 0177332-A 56 18-Oct-2001;
Heska Corporation (US)
Location/Qualifiers
FEATURES
source 1. .620
/organism="Canis familiaris"
/db_xref="taxon:9615"

BASE COUNT 179 a 127 c 102 g 212 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2e-127;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 601 caagatatggactgtgtata 620
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RESULT 3
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LOCUS Canis familiaris interleukin 13 receptor alpha chain 2 (IL13Ra2)
DEFINITION AF314533
ACCESSION AF314533
VERSION AF314533.1 GI:16151870
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1454)

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RESULT 5
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LOCUS AX280327 1454 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 62 from Patent WO0177332.
ACCESSION AX280327
VERSION AX280327.1 GI:16607705
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE McCall,C.A. and Tang,L.
JOURNAL Compositions and methods related to canine igg and canine il-13
receptors
Patent: WO 0177332-A 62 18-OCT-2001;
Heska Corporation (US)
FEATURES
source
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Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 301 gtgaccctgatatttaggttatctctcttgaatggaaccccaattattcccgat 360
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Db 1154 GTGGACCTCGGATATTAGGTTATCTCTTTGCAATGGCAACCTCCATATTTCGGGAT 1095
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Qy 361 aattttaagggaatgcacaataagaatatgaattaaaataccgaacattgatgtaaaac 420
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Db 1094 AATTTTAAGGAATGCACAAATAGATATGAATTAATAATACCGAAACATTTGATAGTGAANAAC 1035
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Qy 421 tggagaaccatcatcaccagaatctacattacaagaatgggttttgatcttacaacaaagt 480
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Db 1034 TGGAGAACCATCATTTACCAAGAATCTACATTTACAAGAATGGGTTTGATCTTTAACAAAGGT 975
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Qy 481 attgaagaagaataaacaacactctgcagacacaatacacaaaatggatgaagttaga 540
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Db 974 ATTGAAGCAAAAGATAAACACACTTCTGCCAGACAATGCACAAATGGATCAGAAGTTAGA 915
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Qy 541 agttcatgggcagaaactacttattggacatcacacagaagaaatcggggaactaaatt 600
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Db 914 AGTTCATGGGCAGAAACTACTTTATTGGACATCACCACAAGGAATTCGGGAACCTAAATTT 855
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Qy 601 caagatatggactgtgtata 620
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Db 854 CAAGATATGGACTGTGTATA 835
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RESULT 6
AX280328
LOCUS AX280328 1158 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 63 from Patent WO0177332.
ACCESSION AX280328
VERSION AX280328.1 GI:16607706
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE McCall,C.A. and Tang,L.
JOURNAL Compositions and methods related to canine igg and canine il-13
receptors
Patent: WO 0177332-A 63 18-OCT-2001;
Heska Corporation (US)
FEATURES
source
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/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 380 a 201 c 224 g 353 t
ORIGIN

Query Match 70.5%; Score 437; DB 6; Length 1158;
Best Local Similarity 100.0%; Pred. No. 5.9e-87;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 atgcttcaattcatcttgatgtcgattctctctatcctctacccgtctgtttgcacagattt 243
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Qy 244 ggcctatgcttcaaatgctgagataaaagttaactctcctcagattttgagatagt 303
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Db 61 GCCTCTATGCTTTCAAAATGCTGAGATAAAAGTTAACTCTCTCAGGATTTTGAGATAGTG 120
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Qy 304 gaccttgatatttaggttatctctcttgaatggcaacctcccatattttcccgataat 363
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Db 121 GACCTCGCATATTAGGTTATCTCTCTTTGCAATGGCAACCTCCCATTTATTTCCGGATAAT 180
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Qy 364 ttaagggaatgcacaataagaatatgaattaaaataccgaacattgatgtaaaactgg 423
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Db 181 TTTAAGGAATGCACAATAGAATATGAATTAATAATACCGAAACATTTGATAGTGAANAACCTGG 240
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Qy 424 aagaccatcattaccaagaattacattacaagaatgggttttgatcttaacaaaggtatt 483
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Qy 484 gaagcaagaataaacacacactcttccagacacaaatgcacaaatggatcgaagttagaagt 543
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Db 301 GAAGCAAGAATAAACACACTTCTGCCAGCACAAATGCACAAATGGATCAGAAAGTTAGAAGT 360
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Qy 544 tcattgggcagaactactatttgacatcaccaagaagaatcggaactcaaaatttcaa 603
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Db 361 TCATGGGCAGAACTACTTATTGGACATCACCAAGGAATCGGGAACCTAAAAATTCAA 420
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Qy 604 gatattggactgtgtata 620
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Db 421 GATATGGACTGTGTATA 437
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RESULT 7
AX280329/c
LOCUS AX280329 1158 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 64 from Patent WO0177332.
ACCESSION AX280329
VERSION AX280329.1 GI:16607707
KEYWORDS
SOURCE
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 64 18-OCT-2001;
Heska Corporation (US)
FEATURES
source
location/Qualifiers
1..1158
/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 353 a 224 c 201 g 380 t
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Query Match 70.5%; Score 437; DB 6; Length 1158;
Best Local Similarity 100.0%; Pred. No. 5.9e-87;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 184 atgctttcattcattggatgcggattcctctatataccctgcttggttgcacagcattt 243
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Db 1158 ATGGCTTTTCATTTCATTTTGGATGTCGGATTCTCTATACCCCTGCTTGTGTCACAGCATTT 1099
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Qy 244 ggcctctatgcttcaaatgcctgagataaagtttaactcctcctcaggattttgagatagt 303
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Db 1098 GGCTCTATGCTTTCAAAATGCTGAGATAAAGTTAATCTCCTCAGGATTTTGAGATAGTG 1039
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Qy 304 gacctggatattaggttatctctcttgcgaatggcaacctccattatttccggataat 363
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Db 1038 GACCTGGATATTAGGTTATCTCTCTTTGCAATGGCAACCTCCATTTATTTCCGGATTAAT 979
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Qy 364 ttttaaggaatgcacaatagataatgaattaaataaccgaaacattgatagtgaaactgg 423
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Db 978 TTTAAGGAATGCACAATAGATAATGAATTAATAATACCGAAACATTTGATAGTGAAACCTGG 919
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Qy 424 aagaccatcattaccaagaattcattacaagaatgggttttgatcttaacaaaggtatt 483
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Db 918 AAGACCATCATTACCAAGAATCTACATTACAAGATGGTTGATCTTAACAAAGGTATT 859
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Qy 484 gaagcaagaataaacacacacttctccagacacaaatgcacaaatggatcagaagttagaagt 543
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Db 858 GAAGCAAGAATAAACACACTTCTGCCAGCACAAATGCACAAATGGATCAGAAAGTTAGAAGT 799
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Db 798 TCATGGGCAGAACTACTTATTGGACATCACCAAGAAATCGGGAACCTAAAAATTCAA 739
Qy 604 gatattggactgtgtata 620
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Db 738 GATATGGACTGTGTATA 722
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RESULT 8
AX280333
LOCUS AX280333 954 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 68 from Patent WO0177332.
ACCESSION AX280333
VERSION AX280333.1 GI:16607711
KEYWORDS
SOURCE
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 68 18-OCT-2001;
Heska Corporation (US)
FEATURES
source
location/Qualifiers
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/translation="MSMSNAEIKVNPDEIIVDPGYLVGLVSLQWOPPLPDPNFKEC
TIEYELAYRNIDSENWTKITIKNLHYKDGFDLNGKIEAKINTFLPDACTNGSEVRSSW
AECTDYIKVNGKNGRCRPFYDLESDDKDFYICVANGSESPQIRPSYIFQLQIVKPM
PPDYLSLTVKNSIEINLKNWPKGPIPAKCFIYEIETEDGTTTWTWTTTVEIEIQTIT
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BASE COUNT 329 a 162 c 192 g 271 t
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Query Match 60.3%; Score 374; DB 6; Length 954;
Best Local Similarity 100.0%; Pred. No. 5.4e-73;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 totatgcttcaaatgcctgagataaaagttaactcctcctcaggttttgagatagtgac 306
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Db 4 TCTATGCTTTCAAAATGCTGAGATAAAGTTAATCTCCTCCTCAGGATTTTGAGATAGTGAC 63
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Qy 307 cctggatattaggttatctctcttgcgaatggcaacctccattatttccggataatttt 366
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Db 64 CTGGATATTAGGTTATCTCTCTTTGCAATGGCAACCTCCATTATTTCCGGATTAATTTT 123
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Qy 367 aaggaatgcacaatagaataatgaataaaataccgaaacattgatagtgaaactgggaag 426
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Db 124 AAGGAATGCACAAATAGATAATGAATTAATAATACCAAAACATTCATAGTGAAACCTGGAA 183
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Qy 427 accatcattaccaagaattcattacaagaatgggttttgatcttaacaaaggtatttaa 486
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Db 184 ACCATCATTTACCAAGAATCTACATTACAAGATGGTTGATCTTTAACAAGATTTGAA 243
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Qy 487 gcaagaataaacacacacttctcgcagacacaaatgcacaaatggatcgaagttagaagtca 546
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Db 244 GCAAGATATAACACACTTCTGCCAGCACAAATGCACAAATGGATCAGAAAGTTAGAAGTTCA 303
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Qy 547 tggcagaagaactactatttgacatcaccaagaagaatcggaactcaaaatttcaaat 606
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Qy 607 atggactgtgtata 620
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JOURNAL Patent: WO 0177332-A 67 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
source 1..1095
/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 328 a 211 c 186 g 370 t
ORIGIN

Query Match 60.3%; Score 374; DB 6; Length 1095;
Best Local Similarity 100.0%; Pred. No. 5.3e-73;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 307 cctggatatttaggttatctctcttgcgaatggaacctccattatttcccgataatttt 366
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Db 1035 CCTGGATATTTAGGTTATCTCTCTTTGCAATGGCAAGCTCCATTTATTTCCGGATAATTTT 976

Qy 367 aaggaatgcacaatagaaatgaattaaaataccgaaacattgatactgaaacctggaag 426
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Qy 427 accatcattaccaagaatctacattacaaagatgggtttgatcttaacaaaggtattgaa 486
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Db 915 ACCATCATTTACCAAGAAATCTACATTACAAAGATGGGTTTGATCTTAACAAAGGTATTGAA 856

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Db 855 GCAAGATAAACAACACTTCTGCCAGCACAATGCACAATGGATCAGAAGTTTGAAGTTCA 796

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Db 795 TGGCGAAGAACTACTTTATGGACATCACCAAGAAATCGGAAACTTAAATTTCAAGAT 736

Qy 607 atggactgtgtata 620
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Db 735 ATGGACTGTGTATA 722
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RESULT 12
AX280336 LOCUS AX280336 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 71 from Patent WO0177332.
ACCESSION AX280336
VERSION AX280336.1 GI:16607714
KEYWORDS
SOURCE doq.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 71 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9615"
1..1686
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/translation="MSMLSNAEIKVNPDPDFEIVDPYLGYSLOWOPLPDPNFKEC
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AECTDYITKVGKNGKGRFPYLESSDYKDFYICVNGSSESQPIRPSYIFQLQIVKPM

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BASE COUNT 513 a 384 c 382 g 407 t
ORIGIN

Query Match 60.3%; Score 374; DB 6; Length 1686;
Best Local Similarity 100.0%; Pred. No. 5e-73;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 307 cctggatatttaggttatctctcttgcgaatggaacctccattatttcccgataatttt 366
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Db 64 CCTGGATATTTAGGTTATCTCTCTTTGCAATGGCAACCTCCATTTATTTCCGGATAATTTT 123

Qy 367 aaggaatgcacaatagaaatgaattaaaataccgaaacattgatactgaaacctggaag 426
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Db 124 AAGGAATGCACAATAGAAATGAATTAATAATACCCGAACATTTGATGTAAGTGAAG 183

Qy 427 accatcattaccaagaatctacattacaaagatgggtttgatcttaacaaaggtattgaa 486
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Db 184 ACCATCATTTACCAAGAAATCTACATTACAAAGATGGGTTTGATCTTAACAAAGGTATTGAA 243

Qy 487 gcaagataaaacacactctcgcagcacaatgcacaatggatcagaagttagaagttca 546
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Db 244 GCAAGATAAACAACACTTCTGCCAGCACAATGCACAATGGATCAGAAGTTTGAAGTTCA 303

Qy 547 tggcgagaaactactatttgacatcaccaagaaatcggaactaaaattcaagat 606
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Qy 607 atggactgtgtata 620
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Db 364 ATGGACTGTGTATA 377
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RESULT 13
AX280338/c LOCUS AX280338 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 73 from Patent WO0177332.
ACCESSION AX280338
VERSION AX280338.1 GI:16607716
KEYWORDS
SOURCE doq.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 73 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
source 1..1686
/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 407 a 382 c 384 g 513 t
ORIGIN

Query Match 60.3%; Score 374; DB 6; Length 1686;
Best Local Similarity 100.0%; Pred. No. 5e-73;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 247 tctatgcttcaaatgctgagataaaagttaattcctcctcaggattttgagatagtgagac 306
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Db 1683 TCTATGCTTTCAAATGCTGAGATAAAAGCTTAATCCTCCTCAGGATTTTGGAGATAGTGGAC 1624
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Qy 367 aaggaatgcacaatagaatgaattaaataaccgaaacattgtagtgaataactggaag 426
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Qy 427 accatcattaccagaatctacattacaaaagatgggtttgatctttaaacaaggatttga 486
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Qy 607 atggactgtgtata 620
Db 1323 ATGGACTGTGTATA 1310

RESULT 14
AX280345
LOCUS AX280345 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 80 from Patent WO0177332.
ACCESSION AX280345
VERSION AX280345.1 GI:16607723
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
TITLE 1 (sites)
JOURNAL McCall,C.A. and Tang,L.
FEATURES Compositions and methods related to canine igg and canine il-13
source Patent: WO 0177332-A 80 18-OCT-2001;
Heska Corporation (US)
Location/Qualifiers
1..1686
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BASE COUNT 512 a 388 c 379 g 407 t
ORIGIN

Query Match 60.3%; Score 374; DB 6; Length 1686;
Best Local Similarity 100.0%; Pred. No. 5e-73;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 TCTATGCTTTCAAATGCTGAGATAAAAGCTTAATCCTCCTCAGGATTTTGGAGATAGTGGAC 63
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Db 64 CCTGGATATTTAGGTTATCTCTCTTTGCAATGGCAACCTCCATTATTTCCGGATAAATTTT 123
Qy 367 aaggaatgcacaatagaatgaattaaataaccgaaacattgtagtgaataactggaag 426
Db 124 AAGGAATGCCAATAGAATAGTAATTAATAATACCGAACAATGATGATGAAACTGGGAAG 183
Qy 427 accatcattaccagaatctacattacaaaagatgggtttgatctttaaacaaggatttga 486
Db 184 ACCATCATTTACCAAGAATCTACATTACAAAGATGGTTTGATCTTTACAAAGGTATTGAA 243
Qy 487 gcaaaagataaacacactctctccagcacaaatgcacaaatggatcagaagttagaagtcca 546
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Qy 547 tgggcagaaactactatttgacatcaccaagaagaatcgggaaactaaattcaagat 606
Db 304 TGGCAGAAACTACTATTGGACATCACCAAGGAATCGGGAACCTAAATTCAGAT 363
Qy 607 atggactgtgtata 620
Db 364 ATGGACTGTGTATA 377

RESULT 15
AX280347/c
LOCUS AX280347 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 82 from Patent WO0177332.
ACCESSION AX280347
VERSION AX280347.1 GI:16607725
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
TITLE 1 (sites)
JOURNAL McCall,C.A. and Tang,L.
FEATURES Compositions and methods related to canine igg and canine il-13
source Patent: WO 0177332-A 82 18-OCT-2001;
Heska Corporation (US)
Location/Qualifiers
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407 a 379 c 388 g 512 t
BASE COUNT
ORIGIN

Query Match 60.3%; Score 374; DB 6; Length 1686;
Best Local Similarity 100.0%; Pred. No. 5e-73;
Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1623 CCTGGATATTTAGGTTATCTCTCTTTGCAATGGCAACCTCCATTATTTCCGGATAAATTTT 1564
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Db 1503 ACCATCATTTACCAAGAATCTACATTACAAAGATGGTTTGATCTTTACAAAGGTATTGAA 1444
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Qy 487 gaaagataaacacactctgccagcacaaatgcacaaatgaatcagaagttagaattca 546
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Qy 607 atggaactgtgtata 620
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Db 1323 ATGGACTGTGTATA 1310

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OM nucleic - nucleic search, using sw model

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IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	485.2	55.3	928	9	AL562513
C 2	387.8	44.2	676	9	AI798934
C 3	354.4	40.4	954	9	AL525497
C 4	349	39.7	926	10	BE620022
C 5	320.2	36.5	445	9	AW954333
C 6	310.2	35.3	867	10	BF525412
C 7	291	33.1	579	9	AW629184
C 8	286.6	32.6	537	10	BF591502
C 9	262.6	29.9	517	9	AW136614
C 10	252	28.7	365	9	AA298563
C 11	236.6	26.9	715	10	BE788633
C 12	233.8	26.6	506	9	AW236406
C 13	231.4	26.4	479	9	AI358911
C 14	230	26.2	443	9	AA909507
C 15	223.2	25.4	675	10	BE964459
C 16	205.6	23.4	683	10	BG778615
C 17	196	22.3	743	10	BG723203

18	185.2	21.1	396	10	BG190222	BG190222 RST9279 A
19	181.4	20.7	399	10	BG213456	BG213456 RST33062
20	180.6	20.6	403	10	BG201950	BG201950 RST1296
21	180.4	20.5	409	10	BG215092	BG215092 RST34750
C 22	178	20.3	360	9	AA621766	AA621766 af06d10.s
C 23	171	19.5	823	10	BF968964	BF968964 602270160
C 24	164.6	18.7	465	10	BF523126	BF523126 UI-R-C3-s
C 25	158.2	18.0	446	9	AW001800	AW001800 ws05c01.x
C 26	150.4	17.1	465	10	R52796	R52796 yg99f10.s1
C 27	147.2	16.8	658	10	BI828427	BI828427 603078385
C 28	133.4	15.2	755	10	BE619361	BE619361 601473366
C 29	128.2	14.6	341	9	AA921043	AA921043 vy75h06.f
C 30	87.4	10.0	160	9	AI547789	AI547789 UI-R-C3-s
C 31	84.8	9.7	530	12	AZ557979	AZ557979 RPCI-23-1
C 32	69.6	7.9	176	12	AZ108580	AZ108580 RPCI-23-4
C 33	58	6.6	1101	12	CNS0039G	AL063921 Drosophil
C 34	58	6.6	1201	12	CNS016E1	AL106627 Drosophil
C 35	54.2	6.2	469	12	AQ761600	AQ761600 HS_3332_B
C 36	53.2	6.1	987	12	CNS014FQ	AL104456 Drosophil
C 37	53	6.0	928	12	CNS00DKY	AL071865 Drosophil
C 38	52.8	6.0	1043	12	CNS0145P	AL103735 Drosophil
C 39	52	5.9	1101	12	CNS00EVL	AL069706 Drosophil
C 40	50.8	5.8	928	12	CNS00DKY	AL071865 Drosophil
C 41	50.6	5.8	1200	12	CNS016CO	AL106578 Drosophil
C 42	49.8	5.7	1101	12	CNS016L1	AL106896 Drosophil
C 43	49.2	5.6	1101	12	CNS0039G	AL063921 Drosophil
C 44	49	5.6	1101	12	CNS016TX	AL107199 Drosophil
C 45	49	5.6	1201	12	CNS007JU	AL067358 Drosophil

ALIGNMENTS

RESULT 1

AL562513/c

LOCUS AL562513 LTI_NFL003_NBC3 Homo sapiens cDNA linear EST 16-FEB-2001
DEFINITION prime, mRNA sequence.
ACCESSION AL562513
VERSION AL562513.1 GI:12911007
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 928)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

Location/Qualifiers

1..928

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DC012VF21"

/clone_lib="LTI_NFL003_NBC3"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed

by Life Technologies. Contact : Feng Liang Life

Technologies, a division of Invitrogen 9800 Medical Center

Drive Rockville, Maryland 20850, USA Fax : (1) 301 610

8371 Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com"

265 a 186 c 158 g 312 t

BASE COUNT

7 others


```

Db 196 TTAATATTAGTTATTATTGTAACCGGTCTGCTTTTGGTAAGCCAAACCCCTACCCAAAA 137
Qy 715 acgat-----ctttcatacaaaaaaagagtctttcttctcatcaacacacattctgttg 767
Db 136 ATGATTCCAGAAATTTCTGTGATACATGAAGACTTTCCATATCAAGAGACATGCTATTG 77
Qy 768 actgattaaactcttctatgcccagatgtgttaaaatagatgattttataaactgaagct 827
Db 76 ACTCAACAGTTTCCAGTC--ATGCCAAATGTTCAATATGATGATCTCAATAAATGAATTT 19
Qy 828 ttctctcaaatattgaa 844
Db 18 TTATAACGAATGTTGAA 2

RESULT 3
AL525497
LOCUS AL525497 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC012YF21 5
DEFINITION prime, mRNA sequence.
ACCESSION AL525497
VERSION AL525497
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 954)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 954
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC012YF21"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 295 a 172 c 201 g 285 t 1 others
ORIGIN

Query Match 40.4%; Score 354.4; DB 9; Length 954;
Best Local Similarity 84.0%; Pred. No. 4.4e-50;
Matches 400; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 1 caaggaatcgggaactcaaatcaagatatgactgtgtatattacaactggcaatat 60
Db 474 CAAGGAATCCAGAACTAAAGATTGAGGATATGATGCGTATATACAAATGGCAATAT 533
Qy 61 ttactgtctcttggaaacctggcatgggtgtccattttgataccaattaccagttgttt 120
Db 534 TTACTGTCTTCTGGAAACCTGGCATAGGTGTACTTCTTGATACCAATTACAACTTGTT 593
Qy 121 tactgggtatagggcttggaccatcagcagagtgactgattacatcaaggttaatgga 180
Db 594 TACTGGGTATGAGGGCTTGGATCATGCATACAGTGTGTGTGATTACATCAAGGCTGATGGA 653

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Qy 181 aaaaatgggatgcaggtttccctatttggagtcacagactataaagattttcacatc 240
Db 654 CAAAATATAGGATCAGATTTCCCTATTATTGGAGGCATCAGACTATAAAGATTCTATATT 713
Qy 241 tgtttaatgggtcatcagaatccagcctatccagccatcagaccagctatttttttcagctt 300
Db 714 TGTGTTAATGGATCATCAGAGAACAAGCCTATCAGATCCAGTTATTTTACCTTTTCAGCTT 773
Qy 301 caaaatatagttaaacctatgccaccagactaccttagctcttactgtgaaagtccagag 360
Db 774 CAAAATATAGTTAAACCTTTGCCGCCAGTCTATCTTACTTTTACTCGGAGAGTTTCATGT 833
Qy 361 gaaattaaccttgaaatggaaacatgcctaaagagccattccagccaaatgttttatttat 420
Db 834 GAAATTAAGCTGAAATGGAGCATACCTTTGGGACCTATTCCAGCAAGGTGTTTGTATTAT 893
Qy 421 gaaattgaattcacagagagtggtactacttctgggtgactaccacagtttgagaatga 476
Db 894 GAAATTGAGATCAGAGAAGATGATACTACCTTGGTGACTGCTACAGTTGAAATGA 949

RESULT 4
BE620022/c
LOCUS BE620022
DEFINITION 601473366T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876064 3',
mRNA sequence.
ACCESSION BE620022
VERSION BE620022.1 GI:98909060
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 926)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence start: 26
High quality sequence stop: 704.
High quality sequence stop: 704.
FEATURES
Location/Qualifiers
source
1. 926
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3876064"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 271 a 186 c 169 g 300 t
ORIGIN

Query Match 39.7%; Score 349; DB 10; Length 926;
Best Local Similarity 75.5%; Pred. No. 3.6e-49;
Matches 567; Conservative 0; Mismatches 165; Indels 19; Gaps 10;

Qy 39 tgtatattacaactggcaatttttagtctctcttggaaacctggcagctgggtgtccattt 98
Db 764 TCCGTATATTACTATGCCAATATTACTCTGTTCTTGG-AAACCTGGAATAGGTGTACTGTC 706

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Qy 99 tgataccaattaccagttgttttacttgta--tgagggtctggaccattccagcagtggt 156
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Db 705 TGATACCAATTACAACTTGTGTTTACTTGGAACTGAGGCTTGGATCATGCAATACAGTGT 646

Qy 157 actgattacatcaagggttaatggaataaataatggatgaggtgttccctatttgagtgca 216
|||||
Db 645 GTTGATTACATCAAGCGTGATGGCAAAATATAGGATGAGATTTCCCTATTTTGGAGGCA 586

Qy 217 tcagactataaagatttctacatctgtgttaattggttcacagaaatccagccctatcaga 276
|||||
Db 585 TCAGACTATAAAGATTTCTATATTGTTGTTAATGGATCATCAGAGAAACAGCCTATCAGA 526

Qy 277 cccagctatttta-tttttcagcttcaaaatatagtttaaacctatgcccaccagactacct 335
|||||
Db 525 TCCAGTATTATTCACATTTTCAGCTTCAAAATATAGTTAAACCTTTGCCGCCAGCTATCT 466

Qy 336 tagtcttactgtgaagaattccagaggaaattaaacctgaaatggaacatgcctaaaggacc 395
|||||
Db 465 TACTTTTACTCGGAGAGAGTTTCATGTGAAATTAAGCTGAAATGGAGCATACCTTTGGGACC 406

Qy 396 catccagccaa-atgtttcatttatgaattgaattcaacagagagatggtactacttggg 454
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Db 405 TATTCACACAAAGGTGTTTGTATGATAAATGAGATCAGAGAGATGATACCTTTGG 346

Qy 455 tga-ctaccacagttggaatgagatacaaatcacagaacatcaaatgaaagccaaataa 513
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Db 345 TGATCTGCTACAGTTGAAATGAAACATACACCTTGAACAAACAAATGAACCCGACAA 286

Qy 514 ttatgctttttggttaag-aagtaagtgaaatatttattgtctcagatgatgaat-ctgga 571
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Db 285 TTATGCTTTGAGTAAGTAAGCAAGTGAATATTTATTGCTCAGATGACGGAATATTGGA 226

Qy 572 gtgagtgagtgatgaacaatgctggaaagt---gacatatgaagaagaaaccttagtat 628
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Db 225 GTGAGTGAGTGATAAACAATGCTGGGAAGGTGAAGACCTATCGAAGAAAATTTGCTTAC 166

Qy 629 tttcttgataccatttgccttctcacaattttgttggtaataacttgcctgct-t 687
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Db 165 GTTCTGCTGCTACCATTTGGTGTCATCTTAATATTAGTTATATTGTAACCGGTCGCTAT 106

Qy 688 ttgtataagaacaaagggtttactgaaacgat-----ctttacatacaaaaaaagaagt 740
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Db 105 TTGGCTAAGCAACACACCTACCCAAATGATTCAGAAATTTTCTGTGATACATGAAGA 46

Qy 741 ctttctctcatcaagacacattctgtgactc 771
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Db 45 CTTTCCATATCAAGAGACATGAATTTCACTC 15

RESULT 5
LOCUS AW954333 445 bp mRNA linear EST 01-JUN-2000
DEFINITION EST366403 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION AW954333
VERSION AW954333.1 GI:8144016
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 445)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208

Email: johng@tigr.org
Plate: 62
Seq primer: Reverse.
Location/Qualifiers
source 1..445
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGE"
/note="Vector: pBluescriptSKm"
BASE COUNT 137 a 77 c 88 g 143 t
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Query Match 36.5%; Score 320.2; DB 9; Length 445;
Best Local Similarity 82.5%; Pred. No. 3.1e-44;
Matches 367; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 54 gcaatatttagctctcttgaaacacctggcatgggtggtccattttgtatgataccaattacca 113
Db 1 GCAATATTACTCTCTTCTTGGAAACCTGGCATAGGTGACTTCTTGTATACCAATTACAA 60

Qy 114 gttgttttactgggtatgaggccttgaccattcagacagagtgactgattacatcaaggt 173
Db 61 CTTGTTTACTGGTATGAGGCTTGGATCATGCAATTACAGTGTGTTGATCATCAAGGC 120

Qy 174 taatgaaaaaatatgggatcaggtttccctatttggagtcacagactataaagattt 233
Db 121 TGATGGACAAATATAGGATCGAGATTTCCCTATTTTGGAGGCATCAGACTATAAGAGATT 180

Qy 234 ctacatctgtgttaattgggtcatcagaatcccagcctatcagaccagctattttatttt 293
Db 181 CTATATTGTTGTTAATGGATCATCAGAGAAACAGCCTATCAGATCCAGTTTTCACATT 240

Qy 294 tcagcttcaaaatatagtttaaacctatgccaccagactacacattgacttactgtgaagaa 353
Db 241 TCAGCTTCAAAATATAGTTAAACCTTTGCCGCCAGCTATCTTACTTTACTCGGAGAG 300

Qy 354 ttcagagaaataaacctgaaatggaacatgcctaaagaccattccagccaaatgttt 413
Db 301 TTCTATGTAATTAAGCTGAAATGGAGCATACCTTTGGGACCTATTCCAGCAAGGTGTTT 360

Qy 414 catttatgaattgaattcacagaggtggttactacttgggtgactacacagttgagaa 473
Db 361 TCATTATGAAATTTGAGATCAGAGAAAGATGATACCTACCTTGGTGTGCTGCTACAGTTGAAA 420

Qy 474 tgagatacaaatcacaagaacatca 498
Db 421 TGAACATACACCTTGAACAAACA 445

RESULT 6
LOCUS BF525412 867 bp mRNA linear EST 11-DEC-2000
DEFINITION 602069493F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212574
5', mRNA sequence.
ACCESSION BF525412
VERSION BF525412.1 GI:11612773
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 867)
AUTHORS NTH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be


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Db 219 GCTTCTCGCTACCAATTTGGTTTCATCTTAATATTAGTATATATTGTAACCGGTGCTT 160
Qy 688 ttgtataagcaaggcgtttactgaaacagat-----ctttcatcaaaaaaagaagt 740
Db 159 TTGCGTAAGCCAAACACCTACCCAAAATGATTCAGAAATTTTCTGTGATACATGAAGA 100
Qy 741 cttttctctcaagaacacatctgttgactcagtaaccttccagtcatttgccagatggt 800
Db 99 CTTTCCATATCAAGACATGTAATTGACTCAACAGATTTCAGTC--ATGCCAAATGTT 42
Qy 801 aaatatgagtcatttataaactgaagcttt 829
Db 41 CAATATAAATCTCCATAAACTGAATTTTT 13

RESULT 8
BF591502/c 537 bp mRNA linear EST 30-MAR-2001
LOCUS
DEFINITION
  nb599a12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3275807 3'
  similar to SW:II32.HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2
  CHAIN PRECURSOR ;, mRNA sequence.
ACCESSION
  BF591502
VERSION
  BF591502.1 GI:11693826
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 537)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
  Ph.D.
  CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
  Bonaldo, Ph.D.
  CDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL, send email to:
  info@image.llnl.gov
  Seq primer: -40UP from Gibco
  High quality sequence stop: 480.
FEATURES
  source
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  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="IMAGE:3275807"
  /clone_lib="NCI_CGAP_Brn23"
  /tissue_type="glioblastoma (pooled)"
  /lab_host="DH10B"
  /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
  modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
  strand cDNA was primed with a Not I - oligo(dT) primer [5'
  TGTTACCAATCTGAAGTGGGCGCGGCATATCTTTTTTTTTTTTTTTTTTTTTTTT
  T 3']; double-stranded cDNA was ligated to Eco RI
  adaptors (Pharmacia), digested with Not I and cloned into
  the Not I and Eco RI sites of the modified pT73 vector.
  Library is normalized, and was constructed by Bento
  Soares and M.Fatima Bonaldo."
BASE COUNT 161 a 108 c 94 g 170 t 4 others
ORIGIN
  Query Match 32.6%; Score 286.6; DB 10; Length 537;
  Best Local Similarity 74.8%; Pred. No. 1.2e-38;
  Matches 400; Conservative 0; Mismatches 123; Indels 12; Gaps 3;
  Qy 307 atagttaacctatgccaccagctactagtcttactgtgaagaattccagaggaaatt 366
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Db 537 ATAGTTAAACCTTTGCCGCCAGTCTATCTTACTTTTACTCGGAGAGTTTCATGTGAAT 478
Qy 367 aacctgaatggaacatgccttaaaagacccattccagcaaatgtttcatattatgaatt 426
Db 477 AAGCTGNAATGGAGCANACCTTTGGGACCTATTCAGCAAGGTGTTTGATTATGAAT 418
Qy 427 gaattcacagagagtggtactacttgggtgactcacacagttgagaatgagatacaaatc 486
Db 417 GAGATCAGAGAAGATGATACCTTGGTNGCTGTACAGTTGAAATGAAACAGACACC 358
Qy 487 acaagaacatcaaatgaaagccaaataattatcttttggtaagaagtaaatgtaatt 546
Db 357 TTGAAAACAACAATAATGAAACCCGACAATTTATGCTTTGTAGTAAGAAGCAAGTGAAT 298
Qy 547 tattgctcagatgatggaatctggagtgagtgagtgatgatacaaatgctggaaggt--- 603
Db 297 TATTCTCAGATGACGGAATTTGGAGTGAGTGGAGTGATAAACAATGCTGGGAAGGTGAA 238
Qy 604 gacatatggaaggaacaccttagtattttcttgataccatttgccttcttgcctcaattt 663
Db 237 GACCTATCGAAGAAAACCTTGTCTACGTTCTGCTACCATTTGGTTCATCTTAATTA 178
Qy 664 gtttgggtaaaccttgctgctgtttgtataagcaagggttcttactgaaacagat---- 719
Db 177 GTTATATTTGTAACCGGTCTGCTTTTGGTGAAGCCAAACACCTACCCAAAATGATCCA 118
Qy 720 ---ctttcatcaaaaaaagaagttcttttctcatcaagaacacattctgttgcactgtaa 776
Db 117 GAATTTTCTGTGANACATGAAGACTTTCCATATCAAGAGACATGGTATTGACTCAACAG 58
Qy 777 ctttcagcttattgcccagatgttaaatagcttattgaagcttataaactgaagcttttc 831
Db 57 TTTCCAGTC--ATGCCCAAAATGTTCAATATGAGTCTCAATAAATGAAATTTTCC 5

RESULT 9
AW136614/c 517 bp mRNA linear EST 29-OCT-1999
LOCUS
DEFINITION
  UI-H-B11-aco-g-05-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
  IMAGE:2715080 3', mRNA sequence.
ACCESSION
  AW136614
VERSION
  AW136614.1 GI:6140747
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 517)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  The sequence contained an oligo-dT track that was present in the
  oligonucleotide that was used to prime the synthesis of first
  strand cDNA and therefore this may represent a bonafide poly A
  tail. CDNA Library Preparation: M.B. Soares Lab Clone distribution:
  NCI-CGAP clone distribution information can be found through the
  I.M.A.G.E. Consortium/LLNL at:
  www.bio.llnl.gov/bbrp/image/image.html
  Seq primer: M13 Forward
  POLYA=Yes.
FEATURES
  Location/Qualifiers
  1..517
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="IMAGE:2715080"
  /clone_lib="NCI_CGAP_Sub3"
  /lab_host="DH10B (Life Technologies)"
  /note="Vector: pT73D-Pac (Pharmacia) with a modified
  polylinker; Site_1: Not I; Site_2: Eco RI; The
  NCI_CGAP_Sub3 library is a subtracted library derived from

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the NCI_CGAP_Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br23, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Lei2, NCI_CGAP_Brn25, NCI_CGAP_Lu5, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6, NCI_CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI_CGAP_Kid3 pool 1 LAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids 132376-132391), 1456008-1456775, 1500552-1502855; NCI_CGAP_Kid5 pool 1 LAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LAM 3375-3592, 3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439); NCI_CGAP_GC4 pool 1 LAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1 LAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1 LAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

TAG_Lib=NCI_CGAP_Lu5
TAG_TISSUE=lung
TAG_SEQ=CAAC"

BASE COUNT 150 a 102 c 84 g 181 t
ORIGIN

Query Match 29.9%; Score 262.6; DB 9; Length 517;
Best Local Similarity 73.6%; Pred. No. 1.2e-34;
Matches 379; Conservative 0; Mismatches 124; Indels 12; Gaps 3;

Qy 344 ctgtgaagaattcagagaaattacacctgaaatggaacatgccttaaaaggaccattccag 403
Db 517 CTCGGAGAGTTCATGTCGAAATTAAGCTAAATGAGCATACCTTTGGGACCTATCCAG 458

Qy 404 ccaaatgttctattatgaattcaacagagatggttactactctgggtgactacca 463
Db 457 CAAGTGTGTTTATGAAATTGAGATCAGAGAGATGATACCTACCTGGTGCTGTA 398

Qy 464 cagttgagaatgagatacaaatcacaagaacatcaaatgaaagccaaataattatgcttt 523
Db 397 CAGTTGAAATGAAACATACACCTTTGAAACAAACAAATGAAACCCGACAAATATGCTTTG 338

Qy 524 tggtaagaagtaagtaattatttctcagatgatggaatctggagtgagtgagtg 583
Db 337 TAGTAAGAAGCAAGATGAATATTTATTCCTCAGATTCAGCAGATTTGGATGAGTCGAGTG 278

Qy 584 atgaacaatgctggaaggt---gacatggaaggaacaccttagtattttcttgatac 640
Db 277 ATAACAATGCTGGGAAGGTGAAGACCTATTCGAAAGAAACCTTTGCTAGCTTTCTGGCTAC 218

Qy 641 catttgctttgtctcaatattgttttggtaataacttgcctgctttttgtataagcaaa 700
Db 217 CATTTGGTTTCATCTTAATATTAGTTATATTGTAACCGGTCTGCTTTTGGCTAAGCCAA 158

Qy 701 gggctttactgaaacagat-----cttctcaacaaaaaagaagtgcttttctcatcaa 753
Db 157 ACACCTACCCAAAATGATGATCCAGAATTTTCTGTGATACATGAAGACTTTCCATATCAA 98

Qy 754 gacacattctgtgactcagtaactttcagttcttatgccagatgtttaaatagtgctt 813
Db 97 GAGACATGGTATTGACTCAACAGGTTTCCAGTC--ATGCCCAAAATGTTCAATATGAGTCTC 40

Qy 814 attaaactgaagcttttctcacaatattgaataaa 848
Db 39 AATAAACTGAATTTTCTTCGCAAAAAAATAAAAA 5

RESULT 10
LOCUS AA298563
DEFINITION AA298563 HSC172 cells I Homo sapiens cDNA 5' end similar to IL13 receptor (IL13R), mRNA sequence.
ACCESSION AA298563
VERSION AA298563.1 GI:1950896
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens
MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
REFERENCE 1 (bases 1 to 365)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Barle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinko,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungejun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other ESTs: THC194124
Contact: Kerlavage, AR
Bioinformatics for Genomic Research
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavetigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1. 365
/organism="Homo sapiens"
/db_xref="Arcc (Inhost):178283"
/db_xref="taxon:9606"
/clone_lib="HSC172 cells I"
/cell_type="fibroblast"
/cell_line="HSC172 (16PDL)"
/dev_stage="fetal"
/note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI ; Site_2: XhoI"

BASE COUNT 106 a 66 c 69 g 123 t 1 others
ORIGIN

Query Match 28.7%; Score 252; DB 9; Length 365;
Best Local Similarity 86.1%; Pred. No. 8.3e-33;
Matches 290; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

Qy 1 caagagaaatcgggaactaaatccaagatcgactgtgtattatacaactggcaatat 60
Db 15 CAAGGAATCCAGAAACTAAAGTTCCAGGATATGGATTGCGTATATTACAAATGGCAATAT 74

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QY 61 ttagtctgcttggaaacctggcatgggtgccatttggatcaccaattaccagttgttt 120
Db 75 TTTACTCTGTTCTTGGAAACCTGGCATAGGTGTACTTCTTTGATACCAATTACAACCTGTTT 134
QY 121 tactggtatgagggcttgaccattccagcagagtgtaactgattacatcaaggttaatgga 180
Db 135 TACTGGTATGAGGGCTTGGTTCATGTCATTTACAGTGTGTGTTGATTACATCAAGGCTGATGGA 194
QY 181 aaaaatatggatgcaggtttccctatttggagtcacacactataaagatttctacac 240
Db 195 CAAAATATAGGATGTCAGATTTCCCTATTGAGGAGCATCAGATATAAAGATTCTATATT 254
QY 241 tctgttaatgggtcatcagaatccagcctcatcagaccagctatttta-tttttcagct 299
Db 255 TGTGTTAATGGATCATCAGAGNCAAGCCTATCAGATCCAGTATTTCACCTTTTCCAGCT 314
QY 300 tcaaatatagtttaaacctatgccaccagactacett 336
Db 315 TCAAAATATAGTTAAACCTTTGCCGCCAGCTCTATCCT 351

RESULT 11
BE788633 715 bp mRNA linear EST 20-OCT-2000
LOCUS 601475992F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878831 5',
DEFINITION mRNA sequence.
ACCESSION BE788633
VERSION BE788633.1 GI:10209831
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 715)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14W9643 row: g column: 24
High quality sequence stop: 575.
Location/Qualifiers
1..715
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/db_xref="taxon:9606"
/clone="IMAGE:3878831"
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/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
BASE COUNT 229 a 154 c 141 g 191 t
ORIGIN

Query Match 26.9%; Score 236.6; DB 10; Length 715;
Best Local Similarity 76.1%; Pred. No. 2.4e-30;
Matches 372; Conservative 0; Mismatches 104; Indels 13; Gaps 6;

QY 1 caaggaatccggaactaaaattcaagataggactgtgtatattacaaactggaatat 60
Db 195 CAAGGAATCCAGAACTAAAGTTACAGTATGGATTGCTATATTACAAATGGCAATAT 254

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QY 61 ttagtctgcttggaaacctggcatgggtgccatttggatcaccaattaccagttgttt 120
Db 255 TTTACTCTGTTCTTGGAAACCTGGCATAGGTGTACTTCTTTGATACCAATTACAACCTGTTT 314
QY 121 tactggtatgagggcttgaccattccagcagagtgtaactgattacatcaaggttaatgga 180
Db 315 TACTGGTATGAGGGCTTGGTTCATGTCATTTACAGTGTGTGTTGATTACATCAAGGCTGATGGA 374
QY 181 aaaaatatggatgcaggtttccctatttggagtcacacactataaagatttctacac 238
Db 375 CAAAATATAGGATGTCAGATTTCCCTATTGAGGAGCATCAGATATAAAGATTCTATATT 434
QY 239 ---tctgttaatgggtcatcagaatccagcctcatcagaccagctatttt-tattttt 294
Db 435 TTTGCTGTTTACACTGGATCATCAGAGAACCAAGCCTATCAGATCCAGTATTATTTCCACTTTT 494
QY 295 cagcttcaaa---atatgttaaacctatgccaccagactaccttagtcttactgtgaag 351
Db 495 CAGCTTCAAAACATATACGCTTAAACCTATGCCGCCAGTCTATCTTACTTAAACTCGGGAG 554
QY 352 aattcagaggaataaactgaaatggaaatgcacatgcctaaagga---cccattccagccaaa 408
Db 555 AGTTTCATGTGAAATTAAGCTGACATGGGAGCATACCTACGGAGACCTATCCACCAGGT 614
QY 409 tgttcatttatgaattgaattcacagaggtggtgactacttggtg-actaccacagt 467
Db 615 GCTACCGCATCATGACATTCGGATCAGAGAAGATGATACCTACCTGGTGAACCTGCTACAGT 674
QY 468 tgagaatga 476
Db 675 CGAAATATGA 683

RESULT 12
AW236406/c
LOCUS
DEFINITION AW236406 506 bp mRNA linear EST 13-DEC-1999
x015g12.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2704102 3',
similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2
CHAIN PRECURSOR ;, mRNA sequence.
ACCESSION AW236406
VERSION AW236406.1 GI:6568795
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 506)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyT not found
Seq primer: -400p from gibco
High quality sequence stop: 407.
Location/Qualifiers
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/clone="IMAGE:2704102"
/clone_lib="NCI_CGAP_Ut2"
/cisue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
FEATURES
source

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/lab_host="DH10B"
/Note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
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Best Local Similarity 74.3%; Pred. No. 8e-30;
Matches 365; Conservative 0; Mismatches 112; Indels 14; Gaps 5;
Qy 363 aattaacatgaaatgcctaaaggagcccaattccagccaaattttcattatga 422
Db 487 AATTAAAGCTGAATGGAGCAACCCCT-TGGGACCTATTCCAGCAAGGTGTTGGATTATGA 429
Qy 423 aatgaattcacagaggatgactactctggtgactaccacagtggaatgagataca 482
Db 428 AA-TGAGATCAGAGAAGATGATACCTTGGTGACTGTACAGTTGAGATGAACATA 370
Qy 483 aatcacaagaacatcaaatgaaagccaaattatgctttttggtgaagaatgaaatgaa 542
Db 369 CACCTTGAACACAAATGAACCCGACATATTATGCTTTGTAGTAAGCAAGCAAGTGA 310
Qy 543 tattattgctcagatgaaatctgagtgagtgagtgagtgagtgagtgagtgagtgagtg 602
Db 309 TATTTATTGCTCAGATACGGAATTTGGAGTGAGTGAGTGAGTAAACAATGCTGGGAAG 250
Qy 603 t---gacatatgaaaggaaccccttagtatttttttctgataccattgtttgtctcaat 659
Db 249 TGAAGACCTTATGAAGAAACCTTCTACGTTCTGGCTACCATTTGGTTTCATCTTAAT 190
Qy 660 attgttttggttaataactgctgctgtttgtataagcaagggtcttactgaaacagat 719
Db 189 ATTACTTATATTGTAACCGGCTCTCTTTTGGTAAGCCAAACACACTACCCAAAATGAT 130
Qy 720 -----cttttcatacaaaaaaagtgcttttcttcatacaagacacactctgttgactca 772
Db 129 TCCAGAAATTTTCTGTGATACATGAAGACTTTCCATATATCAAGAGACATGGTATTGACTCA 70
Qy 773 gtaacttcagctcttatgagcagatgttaaatatagctcttattaaactgaagctttccc 832
Db 69 ACAGTTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATAACTGAATTTTCTT 12
Qy 833 tcaaatattga 843
Db 11 GCGAATGTAA 1

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RESULT 13
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LOCUS qy19c05.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2012456 3'
DEFINITION similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2
CHAIN PRECURSOR ; mRNA sequence.
ACCESSION AI358911
VERSION AI358911.1 GI:4110532
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 479)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.

```

```

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bbrp/image/image.html
Insert Length: 1039 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 324.
FEATURES
Location/Qualifiers
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/lab_host="DH10B"
/note="Organ: brain; Vector: p773D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCCGATATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      144 a      98 c      79 g      157 t
ORIGIN
Query Match      26.4%; Score 231.4; DB 9; Length 479;
Best Local Similarity 73.7%; Pred. No. 2.1e-29;
Matches 351; Conservative 0; Mismatches 112; Indels 13; Gaps 4;
Qy 364 attaacctgaaatgaaacatgctaaaggagcccaattccagccaaattttcattatga 423
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Qy 424 attgaattcacagaggatggtactctggtgactaccacagtgagtgagtgagtgagtgag 483
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Qy 484 atcacaagaacatcaaatgaaagccaaatattgcttttggtaagaagtgaatgaat 543
Db 360 GCCTTGAACAAACAAATGAAACCCGACAAATATGCTTTGTAGTAAGAGCAAGTGAAT 301
Qy 544 atttattgctcagatgaggaatctgagtgagtgagtgagtgagtgagtgagtgagtgag 603
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Qy 604 ---gacatatgaaaggaaccccttagtatttttcttgataccattgttcttctcaata 660
Db 240 GAAGACCTATCAGAGAAACTTTGTACGTTTCTGGCTACCATTTGGTTTCATCTTAATA 181
Qy 661 ttgttttggttaataactgctgctgtttgtataagcaagggtcttactgaaacagat- 719
Db 180 TTAGTTATATTGTAACCGTCTGCTTTTGGTAAGCCAAACACCTTACCCAAAATGATT 121
Qy 720 -----cttttcatacaaaaaaagtgcttttcttcatacaagacacactctgttgactcag 773
Db 120 CCAGAAATTTTCTGTGATACATGAAGACTTTCCATATATCAAGAGACATGGTATTGACTCAA 61
Qy 774 taacttcagctcttatgagcagatgttaaatagctcttattaaactgaagctttt 829
Db 60 CAGTTTCCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATAAATGAATTTT 7
RESULT 14
AA909507/c AA909507 443 bp mRNA linear EST 23-JUN-1998
LOCUS oltedil.sl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1523637 3' similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13

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Db 430 AAGATGATACACCTGGTGTGACTGCTACCAAGTTGAAATGAAACATACCACCCCTTGGAAA 371
Qy 496 tcaaatgaaag-----ccaaaaattatgcttttttggtaaaga--gtaagtgaaatatitta 548
Db 370 CCCACCAATGGAACCCCGACCAATTATGCTTTGTAGTAAGAACGGCCCAAGTGAATATTTA 311
Qy 549 ttgct-cagatgatggaatctggagtgagtgagtgatgaacaatgctggaaggt---g 604
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Qy 605 acatatgaaggaacacctagtttttcttgataccatttgcttttctcaatatitg 664
Db 250 ACCATCGAAGAAACTTTGCTACGTTTCTGGCTACCCCTTTGGTTTCATCTTAATATTAG 191
Qy 665 ttttggtataaacttgctgctgttttgataagcaagggttttactgaaa-----acga 718
Db 190 TTATATTGTAAACCGTCTGCTTTTGGCGTAAGCCCGCACACCTTACCCCGCAATGATCCCGA 131
Qy 719 tcttcatacaaaaaaagaagctcttttctcatcaagacacacattctgttgactcagtaact 778
Db 130 ATTTTCTGTGATACATGAAGACTTTCCATATCCAGACACCTGGTATTGACTC-CACCGT 72
Qy 779 ttcagttctatggccagatgttaaatatagttcttattaaactgaagcttttccctcaaat 838
Db 71 TTCCGGATCATGGCCCAATGTTCCATATGAGTTTCCATAAACTGAATTTTCTTGGCGAAA 12
Qy 839 attgaataaa 848
Db 11 AAAAAAAAAA 2

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 Job time: 9705 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 13:35:56 ; Search time 108.29 Seconds
(without alignments)
1991.562 Million cell updates/sec

Title: US-09-828-995B-57
Perfect score: 878
Sequence: 1 caaggaaatcgggaactaa.....aaangaaaaaaaaaaaaa 878

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533.6	60.8	1369	1	US-08-609-572-3
2	533.6	60.8	1369	4	US-08-841-751-3
3	533.6	60.8	1369	4	US-08-846-340-3
4	533.6	60.8	1369	4	US-08-846-344-3
5	446	50.8	1525	1	US-08-609-572-1
6	446	50.8	1525	4	US-08-841-751-1
7	446	50.8	1525	4	US-08-846-340-1
8	446	50.8	1525	4	US-08-846-344-1
9	42.2	4.8	7218	1	US-08-232-463-14
10	40	4.6	7400	1	US-08-261-663A-1
11	40	4.6	7400	5	PCT-US95-07754A-1
12	38.4	4.4	731	1	US-08-451-405A-2
13	38.4	4.4	3355	2	US-08-933-821-3
14	38.4	4.4	3355	3	US-08-960-507-3
15	38.4	4.4	3355	4	US-09-136-828-3
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17	37.4	4.3	1241	1	US-07-593-657-6
18	37.4	4.3	1241	4	US-08-942-012B-3
19	37	4.2	663	4	US-08-998-416-191
20	37	4.2	854	4	US-08-998-416-534
21	37	4.2	860	4	US-08-998-416-287
22	37	4.2	1472	4	US-08-781-420-10
23	37	4.2	1472	4	US-08-781-420-12
24	37	4.2	1472	4	US-08-874-102-10
25	37	4.2	1472	4	US-08-874-102-12
26	37	4.2	1881	4	US-08-874-102-46
27	37	4.2	1881	4	US-08-874-102-48

28 36.4 4.1 789 6 5219739-8 Patent No. 5219739
29 36.2 4.1 1096 1 US-08-525-507-4 Sequence 4, Appli
30 36.2 4.1 3046 1 US-08-525-507-7 Sequence 7, Appli
31 36.2 4.1 4284 1 US-08-525-507-14 Sequence 14, Appli
32 36 4.1 3573 4 US-09-353-585-4 Sequence 4, Appli
33 35.4 4.0 2639 4 US-09-374-135-1 Sequence 1, Appli
34 35.4 4.0 3848 4 US-09-112-096-28 Sequence 28, Appli
35 35.4 4.0 5668 4 US-09-112-096-14 Sequence 14, Appli
36 35.4 4.0 51952 4 US-08-947-823-1 Patent No. 5194596
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38 35 4.0 3138 1 US-07-867-106-4 Sequence 3, Appli
39 34.4 3.9 3126 2 US-08-477-396A-3 Sequence 2, Appli
40 34.2 3.9 518 1 US-08-485-284A-2 Sequence 10, Appli
41 34.2 3.9 3701 4 US-08-845-258-10 Sequence 10, Appli
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ALIGNMENTS

RESULT 1
US-08-609-572-3
; Sequence 3, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/609, 572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A. 32,724
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
US-08-609-572-3

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Query Match 60.8%; Score 533.6; DB 1; Length 1369;
Best Local Similarity 78.9%; Pred. No. 4.4e-126;
Matches 677; Conservative 0; Mismatches 169; Indels 12; Gaps 3;

QY 1 caaggaaatcgggaaactaaattcaagataggactgtgatatcaaacctggcaaat 60
DB 499 CAAGGAATCCAGAACTAAAGTTCAGGATATGGATTCGGTATATACAAATGGCAATAT 558
QY 61 ttactgtctcttggaaacctggatgggtccattttgtatccaaattaccagttgttt 120
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RESULT 2

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US-08-841-751-3
; Sequence 3, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
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; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
; US-08-841-751-3
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Query Match 60.8%; Score 533.6; DB 4; Length 1369;
Best Local Similarity 78.9%; Pred. No. 4.4e-126;
Matches 677; Conservative 0; Mismatches 169; Indels 12; Gaps 3;

QY 1 caaggaaatcgggaaactaaattcaagataggactgtgatatcaaacctggcaaat 60
DB 499 CAAGGAATCCAGAACTAAAGTTCAGGATATGGATTCGGTATATACAAATGGCAATAT 558
QY 61 ttactgtctcttggaaacctggcagtggtgtccattttgtatccaaattaccagttgttt 120
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QY 121 tactgtgtatggggttggaccattcagcagagtgtactgattacatacaaggtttaatga 180
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QY 301 caaaaatataggatgcaggtttccctattttgagtgatcagacataaaagattttcacatc 360
DB 799 CAAAATATAGTATAAACCCTTTGCCGCCAGTCTATCTTACTTTTACTCGGAGAGATTCATGT 858
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Db 979 TACACCTTGAAACACAACAAATGAACCCGACAATATGCTTTGTAGTAAGAAGCAAAAGTG 1038
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Db 1337 TTGCGAAAAAATAAAAAA 1354

RESULT 3
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; Sequence 3, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
; US-08-846-340-3
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Query Match 60.8%; Score 533.6; DB 4; Length 1369;
Best Local Similarity 78.9%; Pred. No. 4.4e-126;
Matches 677; Conservative 0; Mismatches 169; Indels 12; Gaps 3;

Qy 1 caaggaatcggaacataaattcaagatatgactgtgtatattacaactggcaatat 60
Db 499 CAAGGAATTCAGAAACTTAAAGTTCAGGATATGGATTGCGTATATTACAATGGCAATAT 558
Qy 61 ttactgtctcttggaaacctggcatgggtgtccattttgataccaaattaccagttgttt 120
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Db 979 TACACCTTGAAACACAACAAATGAACCCGACAATATGCTTTGTAGTAAGAAGCAAAAGTG 1038
Qy 541 aatatttatgctcagatgaggaatctggaagtgaagtggagtgatgaacaatgctgaaaa 600
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; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
; US-08-609-572-1

Query Match 50.8%; Score 446; DB 1; Length 1525;
Best Local Similarity 71.5%; Pred. No. 6.3e-104;
Matches 631; Conservative 0; Mismatches 241; Indels 11; Gaps 3;

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Qy 182 aaatatggatgcagggttccctatttggagtcacagcattataaagatttctacatct 241
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Db 935 AAAATATAGTAAACCATGGCCACCAGAAATTCCTTCATATATTAGTGGAGAATTCATG 994
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Db 995 ATATTAGATGAATGGAGCACACCTGGAGGACCATTCCACCAGGTGTACACTATG 1054
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Db 1295 TCCTTTGTACTTCTTTTGCCTTATTTGGAGAAAGAAACCTCAACCCACATTTGAGCC 1354
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Qy 776 acttcagctcttatggccagatgttaaatatgagctcttatttaaacatgaagcttttctca 835
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Qy 836 aaattgtaataacttatttttaaaangaaaaaagaaaaaagaaaaa 878
Db 1470 AATTTGGAATACATCTTCTTGAAATTCCAAAAAAAGAAAAA 1512

RESULT 8

US-08-846-344-1
; Sequence 1, Application US/08846344
; Patent No. 6268480
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846.344
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
US-08-846-344-1

Query Match 50.8%; Score 446; DB 4; Length 1525;
Best Local Similarity 71.5%; Pred. No. 6.3e-104;
Matches 631; Conservative 0; Mismatches 241; Indels 11; Gaps 3;

Qy 2 aaggaaatcggaactaaatcaagatatggaactgtgtatattacaactggcaatt 61
Db 635 AAGGAAGTTTGGAAACTAAATTCAGGCATGAAGTGTATATTATAACTGGCAGTAT 694
Qy 62 tagtctgtcttggaaactggcatgggtgccatttggatccaattaccagtgttt 121
Db 695 TGGTCTGCTCTTGGAAACCTGGCAAGACAGTATATTCTGATACCAACTATACCATGTTT 754
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Db 755 TCTGTGTAGAGGCTTGGATCATGCTTACAGTGTCTGCTATTACCTCCAGCATGATGAA 814
Qy 182 aaatatggatgcagggtttccctatttggagtcactcagactataaagattctcaatc 241
Db 815 AAAATGTTGGATGCAAACTGTCCAACCTTGGACTCATCAGACTATAAAGATTTTATCT 874
Qy 242 gtgttaatgggtcatcagaatcccaagcctcatcagaccagctattttttcagcttc 301
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Qy 302 aaatatagttaaacctatgccaccagacactaccttagtcttactgtgaagaattccagag 361
Db 935 AAAATATAGTTAAACCATTTGCCACCAGAAATTCCTTCATATTAGTGGGAGAAATTCATG 994
Qy 362 aaattaacatgaattggaacatgcctaaaggaccattccagccaaatgtttcattatg 421
Db 995 ATATTAGAATGAATGGAGCACACCTGGAGGACCCCATTCACCAAGGTGTACACTATG 1054
Qy 422 aaattgaattcacagagatggtactacttgggtgactaccacagttgagaatgagatc 481
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Qy 482 aaatcacagaacatcaaatgaagccaaataattatgcttttttgtaagaagtaagtg 541
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Qy 542 atattattgtccagatgatgaattcgtgagtgagtgagtgatgaacaatcgtggaag 601
Db 1175 ATATATATTGTGCAGATGGAATTTGGAGCGAATGGAGTGAAGAGGAATTTGGGAG 1234
Qy 602 gtgacatatgaagaacaccttagtatttttttttttttttttttttttttttttttt 661
Db 1235 GTTACACAGGGCCAGACTCAAAAGATATTATTCATAGTACCAGTTGTCTTTTCTTTATAT 1294
Qy 662 ttgttttgtaataacttgcctgcttttgataaagcaaaaggccttttactgaaacgatc 721
Db 1295 TCCTTTGTACTTCTTTTGCCTTATTTGGAGAAAGAAACCTCAACCCACATTTGAGCC 1354
Qy 722 ttc-----atacaaaaaaagaagctctttctcatcaagacacattctgtgactcag 775

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Db 1355 TCCATGTGGATCGAACAAAGGTGTGCTTATGAAGATACCCCTGTGTTAAACACCA 1414
Qy 776 accttcagctcttattgagcagatttaaatgagctcttattaaactgaagcttttcctca 835
Db 1415 ATTTCTTGACATGAGAGCAG-----CCAGCAGGAGTCATATTAAACTCAA-TTTCCTCTTAA 1469
Qy 836 aatattgataaatcttatttttaaaangaaaaaasaaaaa 878
Db 1470 AATTTCGAATACATCTTCTTGAAATCCAAAAAATAAAAAA 1512

RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; City: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match 4.8%; Score 42.2; DB 1; Length 7218;
Best Local Similarity 2.7%; Pred. No. 0.12;
Matches 8; Conservative 171; Mismatches 114; Indels 0; Gaps 0;

Qy 327 agactacccttactgtgaagaattcagaggaaattaacctgaatggaacatgcc 386
Db 1449 AGAACAATTGTGACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1390
Qy 387 taaagaccattccagccaatgttctattatgaattcagaggaggtgtac 446
Db 1389 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1330
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Qy 447 tacttggtgactaccacagttgaaatgagatcacaaatcacagaacacatcaaatgaaag 506
Db 1329 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1270
Qy 507 ccaaaaattatgcttttggtaagaagtaagtgaaattatttctcagatgaggaat 566
Db 1269 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1210
Qy 567 ctggagtgagtgagtgatgaacaatgctggaaagtgacatgatgaaaggaaa 619
Db 1209 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1157

RESULT 10
US-08-261-663A-1
; Sequence 1, Application US/08261663A
; Patent No. 5571706
; GENERAL INFORMATION:
; APPLICANT: Baker, Barbara J
; APPLICANT: Whitham, Steven A
; TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Margaret A. Connor, USDA-ARS
; STREET: 800 Buchanan Street
; City: Albany
; STATE: CA
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261.663A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Connor, Margaret A
; REGISTRATION NUMBER: 30043
; REFERENCE/DOCKET NUMBER: 0094.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 559-6067
; TELEFAX: (510) 559-5777
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana glutinosa
; TISSUE TYPE: leaf
; FEATURE:
; NAME/KEY: exon
; LOCATION: join(294..772, 1003..2098, 2941..3213, 5032..6600,
; LOCATION: 6934..6951)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 773..1002
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2099..2940
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3214..5031
; FEATURE:
; NAME/KEY: intron
; LOCATION: 6601..6933
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: join(294..772, 1003..2098, 2941..3213, 5032..6600,
; LOCATION: 6934..6951)
US-08-261-663A-1

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Db 2635 TAACATCAGTATTTCTTAAAGAAATCCAAATTAACATTTGATCTTAAACTTTGGTATGCT 2694
Qy 633 ctgtataccatttgccttttgcctcaatatttggtaataacttgcctgcttttga 692
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Qy 693 taagcaaaagggcttactgaaacagatcttctc 724
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RESULT 11
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; Sequence 1, Application PC/TUS9507754A
; GENERAL INFORMATION:
; APPLICANT: Baker, Barbara J
; APPLICANT: Whitham, Steven A
; TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Margaret A. Connor, USDA-ARS
; STREET: 800 Buchanan Street
; CITY: Albany
; STATE: CA
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07754A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Connor, Margaret A
; REGISTRATION NUMBER: 30043
; REFERENCE/DOCKET NUMBER: 0094.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 559-6067
; TELEFAX: (510) 559-5777
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7400 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana glutinosa
; TISSUE TYPE: leaf
; FEATURE:
; NAME/KEY: exon
; LOCATION: join(294..772, 1003..2098, 2941..3213, 5032..6600,
; LOCATION: 6934..6951)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 773..1002
; NAME/KEY: intron
; LOCATION: 2099..2940
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3214..5031
; FEATURE:
; NAME/KEY: intron
; LOCATION: 6601..6933
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(294..772, 1003..2098, 2941..3213, 5032..6600,
; LOCATION: 6934..6951)
PCT-US95-07754A-1

Query Match      4.6%; Score 40; DB 5; Length 7400;
Best Local Similarity 43.9%; Pred. No. 0.42;
Matches 172; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

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Qy 513 attatgcttttggtaagaagtaagtaattatttatttgcagatgatggaactctggag 572
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Db 2635 TAACATCAGTATTTCTTAAAGAAATCCAAATTAACATTTGATCTTAAACTTTGGTATGCT 2694
Qy 633 ctgtataccatttgccttttgcctcaatatttggtaataacttgcctgcttttga 692
Db 2695 AAGCGCTGAGAAAGTAGTGGCCTTATTTCAATTTGACGTGAAGATAGAAATGCCTTTAA 2754
Qy 693 taagcaaaagggcttactgaaacagatcttctc 724
Db 2755 CGACATAAGGGGAAGGGGCAAGAATAAGTTTC 2786

RESULT 12
US-08-451-405A-2/c
; Sequence 2, Application US/08451405A
; Patent No. 5736358
; GENERAL INFORMATION:
; APPLICANT: FASEL, NICOLAS JOSEPH
; APPLICANT: REYMOND, CHRISTOPHE DOMINIQUE
; TITLE OF INVENTION: DICTYOSTELID EXPRESSION VECTOR AND
; TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
; NUMBER OF SEQUENCES: 3
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
2695.824 Million cell updates/sec

Title: US-09-828-995B-57
Perfect score: 878
Sequence: 1 caaggaatcggaactaa.....aaangaaaaaaaaaaaaa 878

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	877	99.9	878	22 AAS59960 Canine interleukin
c 2	877	99.9	878	22 AAS59961 Canine interleukin
3	877	99.9	1454	22 AAS59962 Canine interleukin
c 4	877	99.9	1454	22 AAS59963 Canine interleukin
5	765	87.1	1095	22 AAS59966 Canine interleukin
c 6	765	87.1	1095	22 AAS59967 Canine interleukin
7	765	87.1	1158	22 AAS59968 Canine interleukin
c 8	765	87.1	1158	22 AAS59965 Canine interleukin
9	617.8	70.4	954	22 AAS59968 Canine IL-13R extr

c 10	617.8	70.4	954	22 AAS59969	Canine IL-13R extr
c 11	617.8	70.4	1686	22 AAS59970	Canine IL-13R/IgG-
c 12	617.8	70.4	1686	22 AAS59971	Canine IL-13Ralpha
c 13	617.8	70.4	1686	22 AAS59972	Canine IL-13R/IgG-
c 14	617.8	70.4	1686	22 AAS59973	Canine IL-13Ralpha
c 15	617.8	70.4	1692	22 AAS59974	Canine IL-13R/IgG-
c 16	617.8	70.4	1692	22 AAS59975	Canine IL-13Ralpha
c 17	617.8	70.4	1698	22 AAS59976	Canine IL-13R/IgG-
c 18	617.8	70.4	1698	22 AAS59977	Canine IL-13Ralpha
c 19	534	60.8	1298	18 AAT86464	Human interleukin-
c 20	534	60.8	1298	18 AAT86464	Human interleukin-
c 21	533.6	60.8	1288	19 AAH74791	Nucleotide sequenc
c 22	533.6	60.8	1288	19 AAH74791	Human HR-1 recepto
c 23	533.6	60.8	1288	19 AAH74791	Human cytokine/pep
c 24	533.6	60.8	1369	18 AAT95214	Homo sapiens cDNA
c 25	533.6	60.8	1369	18 AAT95214	cDNA encoding the
c 26	533.6	60.8	1369	21 AAT27912	cDNA encoding IL-1
c 27	533.6	60.8	1369	22 AAS59991	Human interleukin-
c 28	533.6	60.8	1369	22 AAS59993	Human interleukin-
c 29	533.6	60.8	1369	22 AAD02335	Human interleukin
c 30	530.6	60.4	1289	18 AAC81416	Human IL-13 recept
c 31	497.6	56.7	1126	18 AAT96782	Human zcytor2 cyto
c 32	493.2	56.2	1167	18 AAT96783	Celebus macaque zc
c 33	451.6	51.4	947	19 AAV22702	Human zcytor2 cyto
c 34	451.6	51.4	1079	19 AAV22702	Mature interleukin
c 35	451.4	51.4	951	24 AAD22980	Construct containi
c 36	446	50.8	1525	18 AAT95213	Human soluble cyto
c 37	446	50.8	1525	21 AAT27911	cDNA encoding the
c 38	446	50.8	1525	22 AAS59990	cDNA encoding IL-1
c 39	446	50.8	1525	22 AAS59992	Mouse interleukin-
c 40	446	50.8	1525	22 AAD02334	Mouse interleukin-
c 41	446	50.8	1525	22 AAC81415	Murine interleukin
c 42	246	28.0	1539	18 AAT85826	Mouse IL-13 recept
c 43	150.4	17.1	465	19 AAV22698	Human interleukin-
c 44	49.6	5.6	38342	22 AAS46746	Interleukin-13 bin
c 45	46.2	5.3	18598	24 ABL32386	Tumour suppressor
					Human immune syste

ALIGNMENTS

RESULT 1

AAS59960
ID AAS59960 standard; cDNA; 878 BP.

XX AC AAS59960;

XX DT 29-JAN-2002 (first entry)

XX DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 878.

XX DE Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX DE IL-13Ralpha1; IL-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
XX DE immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX DE immune response.

XX OS Canis familiaris.

XX PN WO200177332-A2.

XX XX 18-OCT-2001.

XX XX 09-APR-2001; 2001WO-US11498.

XX PR 07-APR-2000; 2000US-195659P.

XX PR 07-APR-2000; 2000US-195874P.

XX PA (HESK-) HESKA CORP.

XX XX McCall CA, Tang L;

XX XX WPI; 2001-657172/75.

XX DR P-PSDB; AAU69134.

XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
PS
PS
XX Claim 19; Page 170-171; 221pp; English.
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
SQ Sequence 878 BP; 298 A; 141 C; 165 G; 273 T; 1 other;

Query Match 99.9%; Score 877; DB 22; Length 878;
Best Local Similarity 100.0%; Pred. No. 9.6e-193;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 caaggaatcgggaactaaattcaagatatgactgtgactgtatattacaactggcaatat 60
DB 1 caaggaatcgggaactaaattcaagatatgactgtgactgtatattacaactggcaatat 60
QY 61 ttactgtctcttgaaacctggatgggtgtccattttgtatatacaattaccagttgttt 120
DB 61 ttactgtctcttgaaacctggatgggtgtccattttgtatatacaattaccagttgttt 120
QY 121 tactgtgatagggtctggaccattcagcagagtgtactgtattacataaggttaattgga 180
DB 121 tactgtgatagggtctggaccattcagcagagtgtactgtattacataaggttaattgga 180
QY 181 aaaaatatgggatgcaggtttccctatttgagtgatcagactataaagattttcacatat 240
DB 181 aaaaatatgggatgcaggtttccctatttgagtgatcagactataaagattttcacatat 240
QY 241 tgtgttaattgggtcattcagatccagacctatcagaccagctatttttttttcagctt 300
DB 241 tgtgttaattgggtcattcagatccagacctatcagaccagctatttttttttcagctt 300
QY 301 caaaatatagtttaaaccctatgccaccagactaccttagtcttactgtgaagaattcagag 360
DB 301 caaaatatagtttaaaccctatgccaccagactaccttagtcttactgtgaagaattcagag 360
QY 361 gaaattaaacctgaaatggaacatgctctaaaggaccattccagcaaatgtttcatttat 420
DB 361 gaaattaaacctgaaatggaacatgctctaaaggaccattccagcaaatgtttcatttat 420
QY 421 gaaattgaattcacagagatggttactacttgggtgactacacagttgagaatgagata 480
DB 421 gaaattgaattcacagagatggttactacttgggtgactacacagttgagaatgagata 480
QY 481 caaatcaagaacatcaaaatgaaagccaaataattatgcttttggtaagaagtaaatgtg 540
DB 481 caaatcaagaacatcaaaatgaaagccaaataattatgcttttggtaagaagtaaatgtg 540
QY 541 aatattttttgtctcagatgatggaatcctggagtgagtgagtgatgaacaatgctggaaa 600
DB 541 aatattttttgtctcagatgatggaatcctggagtgagtgagtgatgaacaatgctggaaa 600
QY 601 ggtgcacatatggaagaaaccttagtattttttcttgataccaattgtctttgtctcaata 660
DB 601 ggtgcacatatggaagaaaccttagtattttttcttgataccaattgtctttgtctcaata 660
QY 661 ttgtttttggtaaatcacttgctgtctttttgtatagaagcgaagggttttactgaaaacgatac 720

Db 661 tttgttttggttaataacttgctgtcttttgataagcaaaagggttttactgaaaacgatac 720
QY 721 tttcatcaaaaaaagaagtgcttttttctcatcaagacacattctgtgactcagtaactttt 780
Db 721 tttcatcaaaaaaagaagtgcttttttctcatcaagacacattctgtgactcagtaacttt 780
QY 781 cagtcttatgcccagatgttaaatatgactcttattaaactgaagcttttctcacaatat 840
Db 781 cagtcttatgcccagatgttaaatatgactcttattaaactgaagcttttctcacaatat 840
QY 841 tgaataatcttatttttaaaangaaaaaataaaaaaa 878
Db 841 tgaataatcttatttttaaaangaaaaaataaaaaaa 878
RESULT 2
AAS59961/C
ID AAS59961 standard; cDNA; 878 BP.
XX
AC AAS59961;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 878 complement.
KW
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG FC;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US11498.
PF
XX 07-APR-2000; 2000US-195659P.
PR
XX 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.
XX
PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS Claim 19; Page 172-173; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX
SQ Sequence 878 BP; 273 A; 165 C; 141 G; 298 T; 1 other;

Query Match 99.9%; Score 877; DB 22; Length 878;

Best Local Similarity 100.0%; Pred. No. 9.6e-193;			
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	caaggaatacgggaaactaaatccaagatatggactgtgtatattacaactggcaatat	60
Db	878	CAAGGAATAcGGGAACTAAATCAAGATATGGACTGTGTATATTACAACTGGCAATAT	819
Qy	61	ttagctgtctcttggaaacctggatgggtgtccattttgataccaattaccagttgttt	120
Db	818	TTAGTCTGCTCTTGGAAACCTGGCATGGGTGTCCATTTTGTATACCAATTACCAGTTGTTT	759
Qy	121	tactgggtatagggcttggaccattcagcagagtgactaattacatacaagaattaaatga	180
Db	758	TACTGGGTATAGGGCTTGGACCATTcAGCAGAGTGTACTGTATACATCAAGGTTAAATGGA	699
Qy	181	aaaaatatgggatcagagtttccctatttggagtcacagactataaagatttctacatc	240
Db	698	AAAAATATGGGATCGAGGTTTCCCTATTTGGAGTCATCAGACTATAAAGATTTCTACATC	639
Qy	241	tgtgttaattgggtcatcagaatcccagcctatcagacccagcattttttttttttcagctt	300
Db	638	TGTGTTAATGGGTcATCAGAAATCCAGCTATCAGACCCAGCTATTTTATTTTTCAGCTT	579
Qy	301	caaaatatagttaaacctatccaccagactaccttagtcttactgtgaagaattcagag	360
Db	578	CAAAATATAGTTAAACCTATGCCACAGACTACCTTAGTCTTACTGTGAAGAAATTCAGAG	519
Qy	361	gaattaaacctgaaatgaaacatgcctaaaggaccattccagccaaatgtttcatttat	420
Db	518	GAATTAACCTGAAATGGAACATGCCTAAAGGACCCATTCAGCCAAATGTTTCATTTAT	459
Qy	421	gaattgaattcacagaggtgtgtactacttgggtgactaccacagttgagaatgagata	480
Db	458	GAAATTAATTCACAGAGGTGTACTACTTGGGTGACTACCCAGCTTGAGAATGAGATA	399
Qy	481	caaatcacagaatacaaatgaaagccaaataatgtcttttttgggtgaagaagtaagtg	540
Db	398	CAAAATCAAGAAACATCAAAATGAAAGCCAAAATTTATGCTTTTGGTAAGAAAGTAAAGTG	339
Qy	541	aattattatgtctcagatgaggaatcgtggagtgagtgagtgatgaacaatgctgaaa	600
Db	338	AAATATTTATGCTCAGATGATGGAATCTGGAGTGGAGTGATGAACAATGCTGGAAA	279
Qy	601	ggtgacatatggaaggaaccttagtattttcttgtataccatttgcctttgtctcaata	660
Db	278	GGTGACATATGGAAGAAACCTTAGTATTTTCTGTATACCATTGCTTTGTCTCAATA	219
Qy	661	tttgttttggtaataacttgctgtcttttggataagcaagggttttactgaaacgacatc	720
Db	218	TTTGTGTTTGGTAATAACTTGCTGCTTTTGTATAAGCAAAAGGGCTTTACTGAAAACGATC	159
Qy	721	tttcatcaaaaaaagaagtccttttctcatcaagacacattctgttgactcagtaacttt	780
Db	158	TTTTCATCAAAAAAAGAAGTCTTTCTCATCAAGACACATTTCTGTGTACTCAGTAACCTT	99
Qy	781	cagtccttagccagatgttaaatatagtccttattaaactgaagcttttctcctcaaatat	840
Db	98	CAGTCTTATGGCCAGAGTTPAAATATGAGTCTTATTAACCTGAAGCTTTTCTCTCAATAT	39
Qy	841	tgaataatcttatttttaaaangaaaaaataaaaaa 878	
Db	38	TGAATAAATCTTATTTTAAAAANGAAAAAATAAAAAA 1	

RESULT 3
AAS59962
ID AAS59962 standard; cDNA; 1454 BP.
XX
AC AAS59962;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1454.

XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW Immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN W0200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
PR
XX (HESK-) HESKA CORP.
XX
XX McCall CA, Tang L;
XX
XX WPI; 2001-657172/75.
DR P-PSDB; AAU69135.
DR
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Claim 19; Page 173-175; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins are useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
SQ Sequence 1454 BP; 491 A; 238 C; 282 G; 442 T; 1 other;

Query Match 99.9%; Score 877; DB 22; Length 1454;			
Best Local Similarity 100.0%; Pred. No. 1.1e-192;			
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	caaggaatacgggaaactaaatccaagatatggactgtgtatattacaactggcaatat	60
Db	577	caaggaatacgggaaactaaatccaagatatggactgtgtatattacaactggcaatat	636
Qy	61	ttagctgtctcttggaaacctggcatgggtgtccattttgataccaattaccagttgttt	120
Db	637	ttagctgtctcttggaaacctggcatgggtgtccattttgataccaattaccagttgttt	696
Qy	121	tactgggtatgagggcttggaccattcagcagagtgactgattacatcaaggttaatga	180
Db	697	tactgggtatgagggcttggaccattcagcagagtgactgattacatcaaggttaatga	756
Qy	181	aaaaatatgggatcagagtttccctatttggagtcacagactataaagatttctacatc	240
Db	757	aaaaatatgggatcagagtttccctatttggagtcacagactataaagatttctacatc	816
Qy	241	tgtgttaattgggtcatcagaatcccagcctatcagaccagctatttttttttttcagctt	300
Db	817	tgtgttaattgggtcatcagaatcccagcctatcagaccagctatttttttttttcagctt	876
Qy	301	caaaatatagttaaacctatgccacagactacaccttagtcttactgtgaagaattcagag	360

Db 877 caaataatagttaaaccctatgccaccagactacotttagtcttactgtgaagaattcagag 936
Qy 361 gaaataaacctgaaatggaacatgctctaaaggaccattccagccaaatgtttcattat 420
Db 937 gaaataaacctgaaatggaacatgctctaaaggaccattccagccaaatgtttcattat 996
Qy 421 gaaattgaattcacagagatggtactactctggtgactacacacagttgaaatgagata 480
Db 997 gaaattgaattcacagagatggtactactctggtgactacacacagttgaaatgagata 1056
Qy 481 caaattcacagaacatcaaatgaaaggccaaataattatgcttttggtaagaagtaaaagt 540
Db 1057 caaattcacagaacatcaaatgaaaggccaaataattatgcttttggtaagaagtaaaagt 1116
Qy 541 aatatttattgtctcagatgagtggaatctggaagtgtgagtgatgaacaatgctggaaa 600
Db 1117 aatatttattgtctcagatgagtggaatctggaagtgtgagtgatgaacaatgctggaaa 1176
Qy 601 ggtgacatatggaagaaacaccttagtattttttcttgatacaccattgctttgtctcaata 660
Db 1177 ggtgacatatggaagaaacaccttagtattttttcttgatacaccattgctttgtctcaata 1236
Qy 661 ttgtgttgggttaataactgctgctgttttggataagcaaaagggtctttactgaaacgatac 720
Db 1237 ttgtgttgggttaataactgctgctgttttggataagcaaaagggtctttactgaaacgatac 1296
Qy 721 ttctacacaaaaaagaagtgcttttctcatcaagacacattctgttgactcagtaacctt 780
Db 1297 ttctacacaaaaaagaagtgcttttctcatcaagacacattctgttgactcagtaacctt 1356
Qy 781 cagtccttatggccagatgttaaatgagcttatttataaactgaagcttttctcctcaaatat 840
Db 1357 cagtccttatggccagatgttaaatgagcttatttataaactgaagcttttctcctcaaatat 1416
Qy 841 tgaataaatcttatttttaaaangaaaaaataaaaaa 878
Db 1417 tgaataaatcttatttttaaaangaaaaaataaaaaa 1454
RESULT 4
AAS59963/C
ID AAS59963 standard; cDNA; 1454 BP.
XX AAS59963;
AC AAS59963;
XX 29-JAN-2002 (first entry)
DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1454 complement.
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX Canis familiaris.
OS
XX WO200177332-A2.
PN 18-OCT-2001.
XX 09-APR-2001; 2001WO-US11498.
PF 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX (HESK-) HESKA CORP.
PA McCall CA, Tang L;
XX WPI; 2001-657172/75.
DR Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating

immune response of an animal and for developing regulatory compounds -
Claim 19; Page 177-178; 221pp; English.
The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13R proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence is the reverse complement of a cDNA encoding a protein of the invention.
xx
SQ Sequence 1454 BP; 442 A; 282 C; 238 G; 491 T; 1 other;
Query Match 99.9%; Score 877; DB 22; Length 1454;
Best Local Similarity 100.0%; Pred. No. 1.1e-192;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 caagaaatcgggaaactaaattcaagatatggactgtgtatatatacaactggcaatat 60
Db 878 CAAGAAATCGGAAACCTAAATTCAGATATGGACTGTGTATATTACAACTGGCAATAT 819
Qy 61 ttactgtctcttggaaacctgggaatgggtgtccattttgtatatacaactacagttgttt 120
Db 818 TTACTGTCTCTTGGAAACCTGGCATGGGTGTCCATTTTGATACCAATTACCAAGTTGT 759
Qy 121 tactgtgtatgagggtctggaccattcagcagtgactgtactgtacatcaaggttaagtga 180
Db 758 TACTGGTATAGGGCTTGGACCATTCACACAGTGTACTGTATTACATCAAGGTTAATGGA 699
Qy 181 aaaaataggatgcaggtttccctattttggagtcactcagactataaagatttctacatc 240
Db 698 AAAAAATATGGATGTCAGGCTTTCCCTATTTTGGAGTCATCAGACTATAAAGATTTCTACATC 639
Qy 241 tgtgttaattgggtcactcagaatcccgacctatcagaccagcactattttttttcagctt 300
Db 638 TGTGTTAATGGGTCTCATCAGAAATCCAGCTATCAGACCAGCTATTTTATTATTTTTCAGCTT 579
Qy 301 caaataatagttaaacctatgccaccagactacaccttagtcttactgtgaagaattcagag 360
Db 578 CAAATATAGTTAAACCTATGCCACCAGACTACCTTAGTCTTTACTGTGAAAGAAATTCAGAG 519
Qy 361 gaaatgaacctgaaatggaacatgcctaaaggaccattccagccaaatgtttcatttat 420
Db 518 GAAATTAACCTGAAATGGAACATGCCTAAAGGACCCCATTCACGCCAAATGTTTCATTAT 459
Qy 421 gaaattgaattcacagagatgggtactactctgggtgactacacacagttgaaatgagata 480
Db 458 GAAATTTGAATTCACAGAGGATGGTACTACTTGGGTGACTTACCACAGTTGAGAATGAGATA 399
Qy 481 caaatcacagaacatcaaatgaaaggccaaataattatgcttttggtaagaagtaaaagt 540
Db 398 CAAATCACAGAAACATCAAAATGAAAGCCAAATAATATGCTTTTGGTAAAGAAATGAAATG 339
Qy 541 aatatttattgtctcagatgagtggaatcgtggagtgagtgatgaacaatgctggaaa 600
Db 338 AATATTTATTGCTCAGATGATGGAATCTGGAGTGGAGTGTGATGATGACAAATGCTGGAAA 279
Qy 601 ggtgacatatggaagaaacaccttagtattttcttgatacaccattgctttgtctcaata 660
Db 278 GGTGACATATGGAAGAAACCTTAGTATTTTCTTGATACCAATTTGCTTTTGTCTCAATA 219
Qy 661 ttgttttgggttaataactgctgctgttttggataagcaaaagggtctttactgaaacgatac 720
Db 218 TTTGTTTGGTAATAACTTGCTGCTTTTGTATTAAGCAAGGGCTTTACTGAAACGATC 159

PD	18-OCT-2001.	
XX		
PF		
XX	09-APR-2001; 2001WO-US11498.	
PR	07-APR-2000; 2000US-195659P.	
PR	07-APR-2000; 2000US-195874P.	
XX		
PA	(HESK-) HESKA CORP.	
XX		
PI	McCall CA, Tang L;	
XX		
DR	WPI; 2001-657172/75.	
XX		
PT	Novel isolated canine protein, preferably canine immunoglobulin G	
PT	protein or canine interleukin-13 receptor protein useful for regulating	
PT	immune response of an animal and for developing regulatory compounds	
XX		
PS	Claim 19; Page 183; 221pp; English.	
XX		
CC	The invention concerns an isolated canine protein, preferably canine	
CC	immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)	
CC	receptor protein, the nucleic acids encoding them, antibodies	
CC	raised against them, fusion proteins between the IgG and IL-13 proteins	
CC	and methods of isolating regulators of them. The regulators are useful	
CC	for regulating an immune response in a canine. The proteins useful to	
CC	develop regulatory compounds including inhibitors and activators that,	
CC	when administered to a canine in an effective manner, are capable of	
CC	protecting canine from disease mediated by IL-13Ralpha or IL-13. The	
CC	regulators are useful for treating canine IgG (heavy and/or light chain)	
CC	and/or canine IL-13R mediated responses. The molecules of the invention	
CC	are useful to regulate the immune response of an animal (e.g. by gene	
CC	therapy). The present sequence is the reverse complement of a cDNA	
XX	encoding a protein of the invention.	
XX		
SQ	Sequence 1095 BP; 328 A; 211 C; 186 G; 370 T; 0 other;	
Query Match 87.1%; Score 765; DB 22; Length 1095;		
Best Local Similarity 100.0%; Pred. No. 6.3e-167;		
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 caaggaatcgggaaactaaattcaagatatggactgtgatatatacaactggcaatat 60	
DB	765 CAAGGAAATCGGAAACTAAATTCAGATATGGACTGTGTATATACAACTGGCAATAT 706	
QY	61 ttagctgctcttgaacctggcatgggtgccattttgataccaattaccagttgttt 120	
DB	705 TTAGTCTGCTCTTGAAACCTGGCATGGGTGCCATTTTGATACCAATTACCAAGTTGTTT 646	
QY	121 tactggtatagggtcttgaccattcagcagtgactgtactgattacatcaagggttaattgga 180	
DB	645 TACTGGTATGAGGCTTGGACCATTCAGCAGAGTGTACTGATTACATCAAGGTTAATGGA 586	
QY	181 aaaaatacggatgcaggtttccctatttgagtcacagactcagaactataaagatttcacatc 240	
DB	585 AAAAAATATGGATGTCAGGTTTCCCTATTGGAGTCATCAGACTATAAAGATTTCTACATC 526	
QY	241 tctgtaattgggtcaccgaatccagcctatcagaccagctatttttttcagctt 300	
DB	525 TGTGTTAATGGGTCTATCAGATGCCAGGCTATCAGACCCAGCTATTTTATTTCAGGTT 466	
QY	301 caaaaatagttaaacctatgcaccagactacaccttagtcttactgtgaaagaattcacag 360	
DB	465 CAAAATATAGTTAAACCTATGCCACCAGACTACCTTAGTCTTACTGTGAAGAAATTCAGAG 406	
QY	361 gaaataacctgaaatggacatgcctaaaggaccatccagccaatgttttcattat 420	
DB	405 GAAATTAACCTGAAATGGAACATGCTAAAGGACCCATTCACGCAAAATGTTTCATTTAT 346	
QY	421 gaaattgaattcacagagatgggtactacttgggtgactaccacaggttgagaatagata 480	
DB	345 GAAATTAATTCACAGAGATGGTACTACTTGGGTGCTATCCACAGTTGAGAAATGAGATA 286	
QY	481 caaatcacagaacatcaaatgaaagccaaaattatgcttttttgtaagaagtaaatg 540	
DB	285 CAAATCACAGAACATCAATGAAGCCCAAAATTTATGCTTTTGGTAAAGATGAAGTG 226	
QY	541 aatattattgctcagatgtaggaatcctggagtgagtgagtgatgaacaaatgctggaaa 600	
DB	225 AATATTTTATGCTCAGATGATGAATCTGGAGTGAAGTGAATCAACAATGCTGGAAA 166	
QY	601 ggtgacatatgaagaaacaccttagtatttttcttgatcaccattgttcttcaata 660	
DB	165 GGTGACATATGAAGAAACCTTAGTATTTTCTTGATACCATTTGCTTTTGTCTCAATA 106	
QY	661 ttgttttggttaataactgctgctttttgtatagaagcaggctttactgaaacgattc 720	
DB	105 TTTGTTTGGTAAATAACTTGCCTGCTTTTGTATAGCAAGGGCTTTACTGAAACGATC 46	
QY	721 ttctatacaaaaaaagaagtgcttttctctcatcaagacacattctgt 765	
DB	45 TTTTCATACAAAAAAGAAGTCTTTTCTCATCAAGACACATTTCTGT 1	
RESULT 7		
AAS59964		
ID	AAS59964 standard; cDNA; 1158 BP.	
AC	AAS59964;	
DT	29-JAN-2002 (first entry)	
DE	Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1158.	
KW	Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;	
KW	IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;	
KW	immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;	
XX	immune response.	
OS	Canis familiaris.	
PN	WO200177332-A2.	
XX	18-OCT-2001.	
XX	09-APR-2001; 2001WO-US11498.	
PR	07-APR-2000; 2000US-195659P.	
PR	07-APR-2000; 2000US-195874P.	
XX	(HESK-) HESKA CORP.	
PI	McCall CA, Tang L;	
DR	WPI; 2001-657172/75.	
XX		
PT	Novel isolated canine protein, preferably canine immunoglobulin G	
PT	protein or canine interleukin-13 receptor protein useful for regulating	
PT	immune response of an animal and for developing regulatory compounds	
XX		
PS	Claim 19; Page 178; 221pp; English.	
XX		
CC	The invention concerns an isolated canine protein, preferably canine	
CC	immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)	
CC	receptor protein, the nucleic acids encoding them, antibodies	
CC	raised against them, fusion proteins between the IgG and IL-13 proteins	
CC	and methods of isolating regulators of them. The regulators are useful	
CC	for regulating an immune response in a canine. The proteins useful to	
CC	develop regulatory compounds including inhibitors and activators that,	
CC	when administered to a canine in an effective manner, are capable of	
CC	protecting canine from disease mediated by IL-13Ralpha or IL-13. The	
CC	regulators are useful for treating canine IgG (heavy and/or light chain)	
CC	and/or canine IL-13R mediated responses. The molecules of the invention	
CC	are useful to regulate the immune response of an animal (e.g. by gene	
CC	therapy). The present sequence is the reverse complement of a cDNA	
XX	encoding a protein of the invention.	
XX		

SQ Sequence 1158 BP; 380 A; 201 C; 224 G; 353 T; 0 other;

Query Match 87.1%; Score 765; DB 22; Length 1158;
Best Local Similarity 100.0%; Pred. NO. 6.4e-167;
Matches 765; Conservative 0; Mismatches 0; Indels 0

Qy	1	caaggaatcggaacataaaattcaagatatggaatgtagtatattacaaactggcaatat	60
Db	394		453
		caaggaaatcggaacataaaattcaagatatggaatgtagtatattacaaactggcaatat	
Qy	61	ttagtctgctcttggaaacctggcatgggtggtccatttggataccaaattaccagttgctt	120
Db	454		513
		ttagtctgctcttggaaacctggcatgggtggtccatttggataccaaattaccagttgctt	
Qy	121	tactgggtatgagggcttggaccattcagcagagtgtagtattacatacaaggttaatgga	180
Db	514		573
		tactgggtatgagggcttggaccattcagcagagtgtagtattacatacaaggttaatgga	
Qy	181	aaaaatatgggatacgaggtttccctatttggagtcatacagactataaaagatttcacatc	240
Db	574		633
		aaaaatatgggatacgaggtttccctatttggagtcatacagactataaaagatttcacatc	
Qy	241	tgtgttaatgggttcatacagaatcccagcctatcagaccagactattttatttttcagctt	300
Db	634		693
		tgtgttaatgggttcatacagaatcccagcctatcagaccagactattttatttttcagctt	
Qy	301	caaaatatagtttaaacctatgcccacagactaccttagtcttactgtgaagaattccagag	360
Db	694		753
		caaaatatagtttaaacctatgcccacagactaccttagtcttactgtgaagaattccagag	
Qy	361	gaaattaacctgaaatggaacatgacctaaaggaccattccagccaaaatgtttcatttat	420
Db	754		813
		gaaattaacctgaaatggaacatgacctaaaggaccattccagccaaaatgtttcatttat	
Qy	421	gaaattgaattcacagaggatgtagtactacttgggtgactaccacagttgagaatgagata	480
Db	814		873
		gaaattgaattcacagaggatgtagtactacttgggtgactaccacagttgagaatgagata	
Qy	481	caaatcacagaacatacaaatgaaagccaaaataatgcttttttggtagaagaataaagtg	540
Db	874		933
		caaatcacagaacatacaaatgaaagccaaaataatgcttttttggtagaagaataaagtg	
Qy	541	aatatatttctctcaagatgtagaaatctggagtgagtgagtgatgaacaaatgctgaaa	600
Db	934		993
		aatatatttctctcaagatgtagaaatctggagtgagtgagtgatgaacaaatgctgaaa	
Qy	601	ggtagacatatggaaggaaaccttagtatttttcttgaaccatttgccttttgcctcaata	660
Db	994		105
		ggtagacatatggaaggaaaccttagtatttttcttgaaccatttgccttttgcctcaata	
Qy	661	ttgtttttgtgataaacttgcctgcttttggataaagcaaaaggctttactgaaaacgata	720
Db	1054		111
		ttgtttttgtgataaacttgcctgcttttggataaagcaaaaggctttactgaaaacgata	
Qy	721	tttctacaaaaaaagaagtctttttctctcatcaagacacattctgt	765
Db	1114	tttctacaaaaaaagaagtctttttctctcatcaagacacattctgt	1158

RESULT 8
AAS59965/c
ID AAS59965 standard; CDNA; 1158 BP.

AA AAS59965:

XX
DT 29-JAN-2002 (first entry)

Canine interleukin 13 receptor cDNA nCaIL-13alpha2 1158 complement.

Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
IL-13Ralpha1; IL-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
immunoglobulin light chain; lambda; ss: immunosuppressive gene therapy;

KW immune response.

OS Canis familiaris.

AA
PN WO200177332-A2.

18-OCT-2001.

09-APR-2001: 2001WO-US11498-XX PF

XX
PR 07-APR-2000: 2000US-195659p

PR 07-APR-2000; 2000US-195874P.
yy

PA (HESK-) HESKA CORP.

PI McCall CA, Tang L; vv

DR WPI; 2001-657172/75.

PT Novel isolated canine protein, pref

PT immune response of an animal and fo

PS Claim 19; Page 179; 221pp; English.

The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13R proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence is the reverse complement of a cDNA encoding a protein of the invention.

Sequence 1158 BP: 353 A: 224 C: 201 G: 380 T: 0 other:
XX

Query Match 87.1%; Score 765; DB 22; Length 1158;
Best Local Similarity 100.0%; Pred. NO. 6.4e-167;
Matches 765; Conservative 0; Mismatches 0; Indels 0

Qy 1 caaggaatcgggaaactaaataatcgaagtatcggaactggtgtattatacaactggcaatat 60
Db 765 CAAGGAATCGGGAACATAAATTCAGATATTCGACATGTGTATTTACAACATGGCAATAT 706

Qv 61 ttagtctgactcttqgaaacctqqcatqqggtqtcatttttgataccaattaccaqtqt 120

Db 705 TTAGTCTGCTCTTGGAAACCTGGCATGGGTGTCCATTTTGATACCAATTACCAGTTGTTT 646

Qy 121 tactgatatgaggagcttggaccattcagcagaggtgtactgattacatccaaggttaattga 180

615 TACTGCTATCAGGGCTTCCACCATTCAGCAGCTCTACTGATTACTAAGCTTAATGGA 586

[illegible][illegible][illegible][illegible]

QY 30T yaaaccaaaccyyaaacyyaaaccccaaaccccccaccccccac 420
:

XX OS Canis familiaris.
XX PN WO200177332-A2.
XX PD 18-OCT-2001.
XX PF 09-APR-2001; 2001WO-US11498.
XX PR 07-APR-2000; 2000US-195659P.
XX PR 07-APR-2000; 2000US-195874P.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Tang L;
XX DR WPI; 2001-657172/75.
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Claim 19; Page 187; 221pp; English.
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins are useful
CC to develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
XX encoding a protein of the invention.
XX
XX Sequence 954 BP; 271 A; 192 C; 162 G; 329 T; 0 other;
XX
XX Query Match 70.4%; Score 617.8; DB 22; Length 954;
XX Best Local Similarity 99.7%; Pred. No. 5e-133;
XX Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1 caaggaaatcggaactaaatcaagatatgagctgtgattatattacaactggcaatat 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 ttagtctgtcttggaaacctggcatgggtgtccattttgataccaattaccagttgtt 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 561 TTAGTCTGCTCTTGGAACTGGCATGGGTGTCCTATTGATACCAATTACCAGTTGTT 502
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 121 tacttggtatggggttgaccattcagcagagtgtactgattacatcaaggttaattgga 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 501 TACTGGTATGAGGCTTGACCATTTCAGCAGAGTGTACTGATTACATCAAGTTAATGGA 442
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 181 aaaaatattggatcaggtttccctatttggagtcacagactataaagattctacatc 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 441 AAAAATATGGGATGCGAGTTTCCCTATTGAGAGTATCAGAGTATTAAGATTTCACATC 382
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 tgtgttaattgggtatcagaatccagcctatcagaccagctattttatttttcagctt 300
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 381 TGTGTTAATGGGTATCAGAAATCCAGCTATCAGAGCCAGCTATTTATTTTCAGCTT 322
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 301 caaataatagttaaacctatgccacagactacaccttagtcttactgtgaagaattccagag 360
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 371 CAAAATATAGTTAAACCTATGCCACCAGACTACCTTAGCTCTACTGTGAGAAATTCAGAG 262
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 gaaattaaacctgaatggaacatgcctaaagaccattccagaccgaatgttccatttat 420
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 261 GAAATTAACCTGAAATGGAACATGCTTAAGAGCCCATTCAGCCCAAAATGTTTCATTAT 202
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 421 gaaattgaattcacagagtggtactacttgggtgactaccacacagttgagaatgagata 480
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 201 GAAATTTGAATTCACAGAGAGTGGTACTACTTGGGTGACTACCACAGTTGAGAATGAGATA 142
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 481 caaatcacagaacatcaaatgaaagccaaaattattctcttttggtaagaagtaagt 540
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 141 CAAATCACAGAACAATCAAAATGAAAGCCAAAATTTATGCTTTTGGTAAGAAGTAAAGTG 82
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 541 aatatttattgtcagatggaatctggagtgagtgagtgatgaacaatgctgggaa 600
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 81 AATATTTATTGCTCAGATGATGGAATCTGGAGTGGAGTGATGAACATGCTTGGAAA 22
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 601 ggtgacatatggaaggaacc 621
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 21 GGTGATATCTGGAAGGAACC 1
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
RESULT 11
AAS59970
ID AAS59970 standard; cDNA; 1686 BP.
XX
XX AC AAS59970;
XX DT 29-JAN-2002 (first entry)
XX DE Canine IL-13R/IgG-Fc fusion protein cDNA nCaIL-13Ralpha2-Fc3523 1683.
XX KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX OS Canis familiaris.
XX PN WO200177332-A2.
XX PD 18-OCT-2001.
XX PF 09-APR-2001; 2001WO-US11498.
XX PR 07-APR-2000; 2000US-195659P.
XX PR 07-APR-2000; 2000US-195874P.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Tang L;
XX DR WPI; 2001-657172/75.
XX PS P-PSDB; AAU69138.
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Claim 37; Page 187-190; 221pp; English.
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins are useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
XX Sequence 1686 BP; 513 A; 384 C; 382 G; 407 T; 0 other;
XX SQ

```
Query Match          70.4%; Score 617.8; DB 22; Length 1686;
Best Local Similarity 99.7%; Pred. No. 5.7e-133;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caaggaaatcggaactaaattcaagatatggactgtgtatatatacaactggcaatat 60
Db 334 caaggaaatcggaactaaattcaagatatggactgtgtatatatacaactggcaatat 393

Qy 61 ttagtctctcttggaaacctggagctgggtgtccatttttgataccaattaccagttgttt 120
Db 394 ttagtctctcttggaaacctggagctgggtgtccatttttgataccaattaccagttgttt 453

Qy 121 tactgtatgagggttggacattcagcagagtgtactgattacatcaagggttaattgga 180
Db 454 tactgtatgagggttggacattcagcagagtgtactgattacatcaagggttaattgga 513

Qy 181 aaaaataatggatgcaggtttccctattttgagtcacatcagactataaagattttcacatc 240
Db 514 aaaaataatggatgcaggtttccctattttgagtcacatcagactataaagattttcacatc 573

Qy 241 tgtgttaatgggttcacatccagctcagcagcttatcagaccagctatttttttccagctt 300
Db 574 tgtgttaatgggttcacatccagctcagcagcttatcagaccagctatttttttccagctt 633

Qy 301 caaaaatagtttaaacctatgccaccagactacaccttagtcttacttctgtaagaattccagag 360
Db 634 caaaaatagtttaaacctatgccaccagactacaccttagtcttacttctgtaagaattccagag 693

Qy 361 gaaataacctgaaatggaacatgcctcaaaaggaccatccagccaaatgttttcatttat 420
Db 694 gaaataacctgaaatggaacatgcctcaaaaggaccatccagccaaatgttttcatttat 753

Qy 421 gaaattgaattcacagaggtggtactacttgggtgactacacagttgagaattgagata 480
Db 754 gaaattgaattcacagaggtggtactacttgggtgactacacagttgagaattgagata 813

Qy 481 caaatccacaagaacatcaaatgaaaggccaaataattatgcttttggtaagaagtaaaagt 540
Db 814 caaatccacaagaacatcaaatgaaaggccaaataattatgcttttggtaagaagtaaaagt 873

Qy 541 aatatatttctgcagatgatggaatctggagtcgagtgagtgatgaaacaatgctggaaa 600
Db 874 aatatatttctgcagatgatggaatctggagtcgagtgagtgatgaaacaatgctggaaa 933

Qy 601 ggtgacatctggaaggaaacc 621
Db 934 ggtgacatctggaaggaaacc 954

RESULT 12
AAS59971/c
ID AAS59971 standard; cDNA; 1686 BP.
XX
AC AAS59971;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine IL-13ralpha2/IgG-Fc fusion protein cDNA reverse complement.
DE
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13ralpha1; IR-13ralpha2; immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
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```
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX (HESK-) HESKA CORP.
XX McCall CA, Tang L;
XX WPI; 2001-657172/75.
XX
PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS Example 4; Page 193-194; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX
SQ Sequence 1686 BP; 407 A; 382 C; 384 G; 513 T; 0 other;

Query Match          70.4%; Score 617.8; DB 22; Length 1686;
Best Local Similarity 99.7%; Pred. No. 5.7e-133;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caaggaaatcggaactaaattcaagatatggactgtgtatatatacaactggcaatat 60
Db 1353 CAAGGAATCGGAAACTAAATTCAGATATGGACTGTGTATATACAACTGGCAATAT 1294

Qy 61 ttagtctctcttggaaacctggagctgggtgtccatttttgataccaattaccagttgttt 120
Db 1293 TTAGTCTGCTCTTGGAAACCTGGCATGGGTGTCCATTTTGATACCAATTAACCAATGTTT 1234

Qy 121 tactgtatgagggttggacattcagcagagtgtactgattacatcaagggttaattgga 180
Db 1233 TACTGGTATGAGGGCTTGGACCATTCAGCAGAGTGTACTGATTACATCAAGGTTAATGGA 1174

Qy 181 aaaaataatggatgcaggtttccctattttggagtcacatcagactataaagattttcacatc 240
Db 1173 AAAAATATGGGATGCAGGTTTCCCTATTGGAGTCATCAGACTATAAGATTTCTTACATC 1114

Qy 241 tgtgttaatgggttcacatccagctcagcagcttatcagaccagctatttttttccagctt 300
Db 1113 TGTGTTAATGGGTTCATCAGAAATCCAGCCTATCAGACCCAGCTATTATTTTTCAGCTT 1054

Qy 301 caaaataatgattaaacctatgccaccagactacaccttagtcttactgtgaaagaattcaga 360
Db 1053 CAAAATATAGTTAAACCTATGCCACCAGACTACCTTAGTCTTACTGTGAAGAAATTCAGAG 994

Qy 361 gaaataacctgaaatggaacatgcctcaaaaggaccatccagccaaatgttttcatttat 420
Db 993 GAAATTAACCTGAATGGAACATGCCTTAAGGAGCCCATTCACAGCCAAATGTTTTCATTAT 934

Qy 421 gaaattgaattcacagaggtggtactacttgggtgactacacagttgagaattgagata 480
Db 933 GAAATTTGAATTCACAGAGGATGGTACTACTTGGGTGACTTACCACAGTTGAGAATGAGATA 874

Qy 481 caaatccacaagaacatcaaatgaaaggccaaataattatgcttttggtaagaagtaaaagt 540
Db 873 CAAATCACAAGAAACATCAAAATGAAAGCCCAAAATATATGCTTTTGGTAAGAAAGTAAGTG 814
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PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds
XX
PS Claim 37; Page 212-213; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX
SQ Sequence 1686 BP; 407 A; 379 C; 388 G; 512 T; 0 other;

Query Match 70.4%; Score 617.8; DB 22; Length 1686;
Best Local Similarity 99.7%; Pred. No. 5.7e-133;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caaggaatcgggaactaaattcaagatgatggactgtgtattatcaactggcaatat 60
Db 1353 CAAGGAAATCGGGAACCTAAATTCAGATATGGACTGTGTATATACAACTGGCAATAT 1294
Qy 61 ttagtctgtctcttggaaacctggcattggtggtccattttgtatcaccaattaccagttgttt 120
Db 1293 TTAGTCTGCTCTTGAAACCTGGCATGGGTGTCATTTGTATACCAATTACCACTGTTT 1234
Qy 121 tactggtatgagggtctggaccattcagcagagtgctactgattacatcaagggttaattgga 180
Db 1233 TACTGGTATGAGGGCTTGACCACTTCAGCAGAGTGCTACTGATTACATCAAGGTTAATGGA 1174
Qy 181 aaaaatatggatgaggtttccctattttggagtcacagactataaagattttcacatc 240
Db 1173 AAAAATATGGATGAGGTGTTCCCTATTGAGATCATCAGACTATAAAGATTTCACATC 1114
Qy 241 tgtgtaattgggtatcagaaatccagacctatcagaccagctattttttttcagctt 300
Db 1113 TGTGTTAATGGGTCAATCAGATCCAGCCTATCAGACCCAGCTATTATTTTTCAGCTT 1054
Qy 301 caaataatagtttaaacctatgcccacagactacotttagtcttactgtgaagaattcagag 360
Db 1053 CAAATATAGTTAAACCTATGCCACCAGACTACCTTAGTCTTACTGTGAAGAATTACAGAG 994
Qy 361 gaattaaacctgaatggaatgcctaaaggaccattccagccaaatgtttcatttat 420
Db 993 GAAATTAACCTGAATGGAATGGAATGCTTAAAGACCCATTCACGCCAAATGTTTCATTAT 934
Qy 421 gaattgaattcacagaggtatggttacttcttgggtggtactaccacagttgagaatgagata 480
Db 933 GAAATGAATTCACAGAGGATGGTACTACTTGGGTGACTACCACAGTTGAGAAATCAGATA 874
Qy 481 caaatcaagaacatcaaatgaaagcccaaaaattatgctcttttggtaagaagtaagt 540
Db 873 CAAATCACAAGAACAATCAAAATGAAAGCCAAAATTTATGCTTTTGGTAAGAAGTAAAGTG 814
Qy 541 aatatttttctcagatgaggaatctcggagtgtgagtgtgagtgtgaggaatgctggaaa 600
Db 813 AATATTTATTCGTCTAGATGGAATCTGGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAGTGAG 754
Qy 601 ggtgacataggaaggaacc 621
Db 753 GGTGATATCTGGAAGGAACC 733

RESULT 15
AAS59974
ID AAS59974 standard; cDNA; 1692 BP.
XX
AC AAS59974;
XX
XX 29-JAN-2002 (first entry)
XX Canine IL-13R/IgG-Fc fusion protein cDNA nCaIL-13Ralpha2-Fc-B9 1689.
XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG Fc;
XX immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX immune response.
XX Canis familiaris.
XX WO200177332-A2.
XX 18-OCT-2001.
XX
XX 09-APR-2001; 2001WO-US11498.
XX
XX 07-APR-2000; 2000US-195659P.
XX 07-APR-2000; 2000US-195874P.
XX (HESK-) HESKA CORP.
XX
XX McCall CA, Tang L;
XX WPI; 2001-657172/75.
XX P-PSDB; AAU69140.
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
XX protein or canine interleukin-13 receptor protein useful for regulating
XX immune response of an animal and for developing regulatory compounds -
XX
XX Claim 37; Page 200-203; 221pp; English.
XX
XX The invention concerns an isolated canine protein, preferably canine
XX immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
XX receptor protein, the nucleic acids encoding them, antibodies
XX raised against them, fusion proteins between the IgG and IL-13 proteins
XX and methods of isolating regulators of them. The regulators are useful
XX for regulating an immune response in a canine. The proteins useful to
XX develop regulatory compounds including inhibitors and activators that,
XX when administered to a canine in an effective manner, are capable of
XX protecting canine from disease mediated by IL-13Ralpha or IL-13. The
XX regulators are useful for treating canine IgG (heavy and/or light chain)
XX and/or canine IL-13R mediated responses. The molecules of the invention
XX are useful to regulate the immune response of an animal (e.g. by gene
XX therapy). The present sequence encodes a protein of the invention.
XX
XX Sequence 1692 BP; 518 A; 376 C; 385 G; 413 T; 0 other;
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Query Match 70.4%; Score 617.8; DB 22; Length 1692;
Best Local Similarity 99.7%; Pred. No. 5.7e-133;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 301 caaaaatagttaaaacctatgccaccagactacacctagtttactgtgaagaattcagag 360
Db 634 caaaaatagttaaaacctatgccaccagactacacctagtttactgtgaagaattcagag 693
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Job time: 17344 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 15:11:29 ; Search time 5720.3 Seconds
(without alignments) 3211.982 Million cell updates/sec

Title: US-09-828-995B-57
Perfect score: 878
Sequence: 1 caaggaatcggaaactaa.....aaanqaaaaaaaaaaaaa 878

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	877	99.9	878	6	AX280324	Sequence
3	877	99.9	1454	4	AF314533	Canis fam
4	877	99.9	1454	6	AX280325	Sequence
5	877	99.9	1454	6	AX280327	Sequence
6	765	87.1	1095	6	AX280330	Sequence
7	765	87.1	1095	6	AX280332	Sequence
8	765	87.1	1158	6	AX280328	Sequence
9	765	87.1	1158	6	AX280329	Sequence
10	617.8	70.4	954	6	AX280333	Sequence
11	617.8	70.4	954	6	AX280335	Sequence
12	617.8	70.4	1686	6	AX280336	Sequence
13	617.8	70.4	1686	6	AX280338	Sequence
14	617.8	70.4	1686	6	AX280345	Sequence
15	617.8	70.4	1686	6	AX280347	Sequence
16	617.8	70.4	1692	6	AX280342	Sequence
17	617.8	70.4	1692	6	AX280344	Sequence
18	617.8	70.4	1698	6	AX280339	Sequence
19	617.8	70.4	1698	6	AX280341	Sequence
20	548.2	62.4	1382	9	HSU70981	Human inter
21	542.8	61.8	1301	9	BC020739	Homo sapi
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25	533.6	60.8	1369	6	AX280363	Sequence
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29	446	50.8	1525	6	AX280362	Sequence
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31	445	50.7	1417	10	BC003723	Mus muscu
32	432.2	49.2	1567	10	MMU65747	U65747 Mus muscu
33	413	47.0	1938	10	AF448818	Rattus no
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35	155.6	17.7	12289	9	HSDA204F4	Human DNA
36	127	14.5	173675	2	AC103226	Sequence
37	87.2	9.9	219051	2	AC103226	Rattus no
38	77	8.8	1741	5	AF62932	Mus muscu
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40	49.8	5.7	12029	3	AE001385	AF049181 Plasmodiu
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42	49.6	5.6	38342	6	AX344503	Sequence
43	49.6	5.6	135792	2	AP003544	Oryza sat
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ALIGNMENTS

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LOCUS		
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ACCESSION	Sequence 57 from Patent WO0177332.	linear
VERSION	AX280322.1	
KEYWORDS	GI:16607700	
SOURCE	doq.	
ORGANISM	Canis familiaris	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
TITLE	1 (sites)	
	Mccall,C.A. and Tang,L.	
	Compositions and methods related to canine igg and canine il-13	
JOURNAL	receptors	
	Patent: WO 0177332-A 57 18-OCT-2001;	
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GLDHSABCTDYIKVGNKMGCRFPYLESSDYICVNGSSQSPIRPSYFIFOLON
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BASE COUNT 298 a 141 c 165 g 273 t 1 others
ORIGIN

Query Match 99.9%; Score 877; DB 6; Length 878;
Best Local Similarity 100.0%; Pred. No. 1.8e-166;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caagaaatcgggaaactaaattcaagatatggactgtgtattatacaactggcaatat 60
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LOCUS Sequence 59 from Patent WO0177332.
DEFINITION AX280324
ACCESSION AX280324
VERSION AX280324.1 GI:16607702
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 59 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.8e-166;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
LOCUS AX280330 1095 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 65 from Patent WO0177332.
ACCESSION AX280330
VERSION AX280330.1 GI:16607708
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE McCall,C.A. and Tang,L.
JOURNAL Compositions and methods related to canine igg and canine il-13
receptors
PATENT: WO 0177332-A 65 18-OCT-2001;
Heska Corporation (US)
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.1e-144;
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QY 361 gaaattaacctgaaatggaacatgcctaaaggaccattccagccaaatgtttcattat 420
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AX280332/c
LOCUS AX280332 1095 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 67 from Patent WO0177332.
ACCESSION AX280332
VERSION AX280332.1 GI:16607710
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE McCall,C.A. and Tang,L.
Compositions and methods related to canine igg and canine il-13
```

JOURNAL
Patent: WO 0177332-A 67 18-OCT-2001;
Heska Corporation (US)
FEATURES
Source 1..1095
Location/Qualifiers
/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 328 a 211 c 186 g 370 t
ORIGIN

receptors
Patent: WO 0177332-A 67 18-OCT-2001;
Heska Corporation (US)
FEATURES
Source 1..1095
Location/Qualifiers
/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 328 a 211 c 186 g 370 t
ORIGIN

Query Match 87.1%; Score 765; DB 6; Length 1095;
Best Local Similarity 100.0%; Pred. No. 5e-144;
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caagaaatcggaactcaaaattcaaatggaactggaactgtgtatattacaactggcaaat 60
Db 765 CAAGAAATCGGAAACCTAAAATTCAAGATATGGACTGTGTATATTACAACCTGGCAATAT 706

Qy 61 ttagtctgtcttggaaacctgggaactgggtgtccattttgtatccaattaccagttgttt 120
Db 705 TTAGTCTCTCTTGAAACCTGGCATGGTGTCCATTTTGATACCAATTACCAGTTGTTT 646

Qy 121 tactgtgtatggggtcttggaaccttcagcagtggtgtactgattacatcaagggttaattgga 180
Db 645 TACTGGTATGAGGGCTTGGAACCTTCAGCAGAGTGTACTGTATTACATCAAGGTTAATGGA 586

Qy 181 aaaaatatgggatcaggtttccctatttgagtcattcagactacagactataaagattttcacatc 240
Db 595 AAAAATATGGGATGAGGCTTTCCCTATTTTGGAGTGCATCAGACTATAAAGATTTCTACATC 526

Qy 241 tgtgttaattgggttcacagatcccgacctatccagaccagctattttatttttcagctt 300
Db 525 TGTGTTAATGGTGCATCAGAACTCCAGAGCTATCAGACCCAGCTATTTATTATTTCAGCTT 466

Qy 301 caaaatatagttaaacctatgccaccagactacaccttagcttactctgtgaagaattcagag 360
Db 465 CAAAATATAGTTAAACCTATGCCACAGACTACCTTAGTCTTACTGTGAAGAAATTCAGAG 406

Qy 361 gaaattaaacctgaaatggaactgcttaaggaccctatccagcccaaatgttttcatttat 420
Db 405 GAAATTAACCTGAAATGGAACATGCGCTAAAGAGCCCATTTCCAGCCAAATGTTTCAATTAT 346

Qy 421 gaaattgaattcacagaggtgtgtactacttgggtgactacacacagttgagaatgagata 480
Db 345 GAAATTGAATTACAGAGAGTGGTACTACTTGGGTGACTACCACAGTTGAGAAATGAGATA 286

Qy 481 caaatcacagaagacatcaaatgaaagcccaaaaattatgcttttggtaagaagttaaagt 540
Db 285 CAAATCACAGAACATCAAAATGAAAGCCCAAAATTTATGCTTTTGGTAAGAAGTAAAGTG 226

Qy 541 aatatttattgtcagatgaggaactctggagtgagtgagtgagtgagtgagtgagtgagtgagga 600
Db 225 AATATTATTGCTCAGATGATGGAATCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGAA 166

Qy 601 ggtgacatatggaaggaaccttagtatttttcttgatcaccatttgcctttgtctcaata 660
Db 165 GGTGACATATGGAAGAAACCTTAGTATTTTCTTGATACCAATTTGCTTTTGTCTCAATA 106

Qy 661 ttgttttgggtaataacttgcctgctgttttctgtataagcaaaagggcttactgaaaacgac 720
Db 105 TTTGTTTGGTAAATAACTTGGCTGCTTTTGTATAGCAAAAGGGCTTTACTGAAACGATC 46

Qy 721 ttctacaaaaaagaagtgcttttctcatcaagacacattctgt 765
Db 45 TTTCTACAAAAAAGAAGTCTTTTCTCATCAAGACACATTCTGT 1

RESULT 8
AX280328
LOCUS
DEFINITION Sequence 63 from Patent WO0177332.
ACCESSION AX280328

AX280328.1 GI:16607706
SOURCE
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 63 18-OCT-2001;
Heska Corporation (US)
FEATURES
Location/Qualifiers
source 1..1158
/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 380 a 201 c 224 g 353 t
ORIGIN

Query Match 87.1%; Score 765; DB 6; Length 1158;
Best Local Similarity 100.0%; Pred. No. 5e-144;
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caagaaatcggaactcaaaattcaaatggaactggaactgtgtatattacaactggcaaat 60
Db 394 CAAGAAATCGGAAACCTAAAATTCAAGATATGGACTGTGTATATTACAACCTGGCAATAT 453

Qy 61 ttagtctgtcttggaaacctgggaactgggtgtccattttgtatccaattaccagttgttt 120
Db 454 TTAGTCTCTCTTGAAACCTGGCATGGTGTCCATTTTGATACCAATTACCAGTTGTTT 513

Qy 121 tactgtgtatggggtcttggaaccttcagcagtggtgtactgattacatcaagggttaattgga 180
Db 514 TACTGGTATGAGGGCTTGGAACCTTCAGCAGAGTGTACTGTATTACATCAAGGTTAATGGA 573

Qy 181 aaaaatatgggatcaggtttccctatttgagtcattcagactataaagattttcacatc 240
Db 574 AAAAATATGGGATGAGGCTTTCCCTATTTTGGAGTGCATCAGACTATAAAGATTTCTACATC 633

Qy 241 tgtgttaattgggttcacagatcccgacctatccagaccagctattttatttttcagctt 300
Db 634 TGTGTTAATGGTGCATCAGAACTCCAGAGCTATCAGACCCAGCTATTTATTATTTCAGCTT 693

Qy 301 caaaatatagttaaacctatgccaccagactacaccttagcttactctgtgaagaattcagag 360
Db 694 CAAAATATAGTTAAACCTATGCCACCAGACTACCTTAGTCTTACTGTGAAGAAATTCAGAG 753

Qy 361 gaaattaaacctgaaatggaactgcttaaggaccctatccagcccaaatgttttcatttat 420
Db 754 GAAATTAACCTGAAATGGAACATGCGCTAAAGAGCCCATTTCCAGCCAAATGTTTCAATTAT 813

Qy 421 gaaattgaattcacagaggtgtgtactacttgggtgactacacacagttgagaatgagata 480
Db 814 GAAATTGAATTACAGAGAGTGGTACTACTTGGGTGACTACCACAGTTTGAGAATGAGATA 873

Qy 481 caaatcacagaagacatcaaatgaaagcccaaaaattatgcttttggtaagaagttaaagt 540
Db 874 CAAATCACAGAACATCAAAATGAAAGCCCAAAATTTATGCTTTTGGTAAGAAGTAAAGTG 933

Qy 541 aatatttattgtcagatgaggaactctggagtgagtgagtgagtgagtgagtgagtgagtgagga 600
Db 934 AATATTATTGCTCAGATGATGGAATCTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGAA 993

Qy 601 ggtgacatatggaaggaaccttagtatttttcttgatcaccatttgcctttgtctcaata 660
Db 994 GGTGACATATGGAAGAAACCTTAGTATTTTCTTGATACCAATTTGCTTTTGTCTCAATA 1053

Qy 661 ttgttttgggtaataacttgcctgttttctgtataagcaaaagggcttactgaaaacgac 720
Db 1054 TTTGTTTGGTAAATAACTTGGCTGCTTTTGTATAGCAAAAGGGCTTTACTGAAACGATC 1113

Qy 721 ttctacaaaaaagaagtgcttttctcatcaagacacattctgt 765

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Db 1114 TTTTCATCAAAAAAGAGCTTTTCTCATCAAGACACATTCTCT 1158

RESULT 9
AX280329/c
LOCUS AX280329 1158 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 64 from Patent WO0177332.
ACCESSION AX280329
VERSION AX280329.1 GI:16607707
KEYWORDS
SOURCE
ORGANISM
Canis familiaris
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE McCall,C.A. and Tang,L.
JOURNAL Compositions and methods related to canine igg and canine il-13
receptors
Patent: WO 0177332-A 64 18-OCT-2001;
Heska Corporation (US)
FEATURES
source 1..1158
/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 353 a 224 c 201 g 380 t
ORIGIN

Query Match 87.1%; Score 765; DB 6; Length 1158;
Best Local Similarity 100.0%; Pred. No. 5e-144;
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 caaggaatcggaacataaaatcaagatatgagctgtgtattacacacgtgcaatat 60
Db 765 CAAGGAATCGGAAATAAAATTCAGATATGGACTGTGTATATTACAACTGGCATAT 706

Qy 61 ttagtctgtcttggaaacctggcgatgggtgtccattttgataccaattaccagttgtt 120
Db 705 TTAGTCTGCTCTTGGAAACCTGGCATGGTGTCTCCATTTTGATACCAATTAACAGTTGTT 646

Qy 121 tactgtgataggcttggaccattcagcagagtgtactgattacacaaaggttaatgga 180
Db 645 TACTGGTATGAGGGCTTGGACCAATTCACAGAGTGTACTGATTACATCAAGGTTAAATGGA 586

Qy 181 aaaaatgagatcgaggtttccctatttggagtcacagactataaagattttcacatc 240
Db 585 AAAAATATGGATCGAGGTTCCCTATTTTGGAGTCATCAGACTATAAAGATTCTACATC 526

Qy 241 tgtgttaattgggtcatcagaatccagccctatcagaccagctattttttttcagctt 300
Db 525 TGTGTTAATGGTTCATCAGAATCCAGCCTATCAGACCCAGCTATTATTTTTCAGCTT 466

Qy 301 caaaatagttaaacctatgccaccagactacctgtactgttactgtgaagaaatcagag 360
Db 465 CAAAATATAGTTAAACCTATGCCACCAGACTACCTTATGCTTACTGTGAAGAAATTCAGAG 406

Qy 361 gaaattaacctgaaatggaatgcctaaaggacccttccagcgaatgtttcatttat 420
Db 405 GAAATTAACTGAANTGAAACATGCCCTAAAGGACCCATTCAGGCCAATGTTTCATTAT 346

Qy 421 gaaattgaattcacagaggttggtactacttgggtgactaccacagttgagaatgagata 480
Db 345 GAAATTGAATTCACAGAGGTGGTACTTTGGGTGACTACCCAGTTGAGAATGAGATA 286

Qy 481 caaatcaagaacatcaaatgaaagccaaataatttgcgttttggtaagaagttaaagt 540
Db 285 CAAATCAAGAACATCAAAATGAAAGCCAAAATTTATGCTTTTGGTAAGAAGTAAAGTG 226

Qy 541 aattattatgtcagatgatgaatcgagtgagtgagtgatgaacaatgctgaaa 600
Db 225 AATATTATTGCTCAGATGATGGAATCTGGAGTGAGTGGAGTGATGAACAATGCTGAAA 166
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Qy 601 ggtgacatatggaaggaaaccttagtatattttcttgatacaattgttttgcctaata 660
Db 165 GGTGACATATGGAAGAAACCTTAGTATTTTCTTGATACCATTTGCTTGTCTCAATA 106

Qy 661 ttgttttggtaaaccttgctgtcttttgtataagcaaaaggcctttactgaagaacgac 720
Db 105 TTGTGTTTGGTAATAACTTGCCTGCTTTTGTATAGCAAGGGCTTTACTGAAAAACGATC 46

Qy 721 ttctacacaaaaaagaagtcttttcttcatacaagacacattctgt 765
Db 45 TTTTCATACAAAAAAGAAGTCTTTTCTCATCAAGACACATTCTCT 1

RESULT 10
AX280333
LOCUS AX280333 954 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 68 from Patent WO0177332.
ACCESSION AX280333
VERSION AX280333.1 GI:16607711
KEYWORDS
SOURCE
ORGANISM
dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (sites)
TITLE McCall,C.A. and Tang,L.
JOURNAL Compositions and methods related to canine igg and canine il-13
receptors
Patent: WO 0177332-A 68 18-OCT-2001;
Heska Corporation (US)
FEATURES
source 1..954
Location/Qualifiers
/organism="Canis familiaris"
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/notes="unnamed protein product"
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/db_xref="GI:16607712"
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TIEVELKYNRINDSENMKTIITKLNHYKDFDLNKGIEAKINTLLPAQCTNGSEVRSSW
AETTYTSPQGNRETKIODMDCVYVNOYLVCWKPGMGVHFDTNVQLFVWYEGLDHS
ARCTDIKVNKNGMCRFPYLESSDYKDFYVNGSESQIPRPSFIIFOLQNIKAPM
PPDYLSTLVKNSSEINLKNMNPPIPACFIYEIETFDGTWVTTTVEVEIQITRT
SNESQKLCFLVRKVNLYCSDDDGIWSEWSDEQCWKGDINKET"
BASE COUNT 329 a 162 c 192 g 271 t
ORIGIN

Query Match 70.4%; Score 617.8; DB 6; Length 954;
Best Local Similarity 99.7%; Pred. No. 1.0e-114;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caaggaatcggaacataaaatcaagatatgagctgtgtattacacacgtgcaatat 60
Db 334 CAAGGAATCGGAAACATAAAATTCAGATATGGACTGTGTATATTACAACTGGCAATAT 393

Qy 61 ttagtctgtcttggaaacctggcgatgggtgtccattttgataccaattaccagttgtt 120
Db 394 TTAGTCTGCTCTTGGAAACCTGGCATGGTGTCCATTTTGATACCAATTAACAGTTGTTT 453

Qy 121 tactgtgatagggtcttggaccattcagcagagtggtactgattacacaaaggttaatgga 180
Db 454 TACTGGTATGAGGGCTTGGACCATTCAGCAGAGTGACTGATTACATCAAGTTAATGGA 513

Qy 181 aaaaatgggatgcaggtttccctatttggagtcacagactataaagattttcacatc 240
Db 514 AAAAATATGGATCGAGGTTTCCCTATTTTGGAGTCATCAGACTATAAAGATTTCATATC 573

Qy 241 tgtgttaattgggtcatcagaatccagccctatcagaccagctattttttttcagctt 300
Db 574 TGTGTTAATGGGTTCATCAGAATCCAGCCTATCAGACCCAGCTATTATTTTTCAGCTT 633
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Qy 301 caaataatagttaaacctatgccaccagactacaccttagtcttactgtgaaagaattcaag 360
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Db 634 CAAAATATAGTTAAACCTATGCCACCAGACTACCTTAGTCTTACTGTGAAGAATTCAGAG 693
Qy 361 gaaattaacctgaatggaacatgcctaaaggaccatccagccaaatgttcatattat 420
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Db 694 GAAATTAACCTGAATGGAACATGCCTAAAGAGCCCATTCAGGCCAAATGTTTCATTTAT 753
Qy 421 gaaattgaattcacagagatgggtactacttgggtgactaccacacagttgagaatgagata 480
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Db 754 GAAATGGAATTCACAGAGGATGGTACTACTTGGGTGACTACCACAGTTGAGAATGAGATA 813
Qy 481 caaatcacagaacatcaaatgaaagccaaataattatgcttttggtaagaagtaaaagt 540
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Db 814 CAAATCAAGAACAATCAAAATGAAAGCCAAATAATTATGCTTTTGGTAAGAAGTAAAGTG 873
Qy 541 aaattatttctcagatgatggaatctggagtgagtgagtgatgatacaaatgctggaaa 600
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Db 874 AATATTTATTGCTCAGATGATGGAATCTGGAGTGGAGTGAGTGAGTGAACAATGCTGGAAA 933
Qy 601 ggtgacatatgaaagaaacc 621
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Db 934 GGTGATATCTGGAAGAAACC 954

RESULT 11
AX280335/c AX280335 954 bp DNA linear PAT 02-NOV-2001
LOCUS
DEFINITION Sequence 70 from Patent WO0177332.
ACCESSION AX280335
VERSION AX280335.1 GI:16607713
KEYWORDS
SOURCE
dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 70 18-OCT-2001;
Heska Corporation (US)
FEATURES
Location/Qualifiers
source 1..954
/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 271 a 192 c 162 g 329 t
ORIGIN
Query Match 70.4%; Score 617.8; DB 6; Length 954;
Best Local Similarity 99.7%; Pred. No. 1.8e-114;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caaggaaatcggaactaaattcaagatatgactgtgtatatcaaacctggcaatat 60
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Db 621 CAAGGAAATCGGAAACTAAAATTAAGATATGAGTGTGTATATTAACAACTGCAATAT 562
Qy 61 ttactgtctcttggaacctggatgggtgctccattttgtatatacaatcaccagttgttt 120
|||||
Db 561 TTAGTCTCTCTTGGAACCTGGCATGGGTGCTCCATTTTGTATACCAATATACCACTGTGTT 502
Qy 121 tactgggtatgaggttgagaccattcagcagatgactgattacatcaaggttaattga 180
|||||
Db 501 TACTGGTATGAGGCTTGGACCATTCACAGAGTGACTGATTACATCAAGGTTAATGGA 442
Qy 181 aaaaatattggatgcaggtttccctattttggagtcacatcagactataaagatttctacatc 240
|||||
Db 441 AAAAATATGGGATGCAGGTTTCCCTATTATTGGAGTCATCAGACTATAAAGATTTCTACATC 382
Qy 241 tgggttaattgggtcatcagaatccagcctatccagaccacagctattttttttcagctt 300
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Db 381 TGTGTTAATGGGTTCATCAGAAATCCAGCCTATCAGACCCAGCTATTTTATTTTTCAGCTT 322
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Qy 301 caaataatagttaaacctatgccaccagactacaccttagtcttactgtgaaagaattcaag 360
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Db 321 CAAAATATAGTTAAACCTATGCCACCAGACTACCTTAGTCTTACTGTGAAGAATTCAGAG 262
Qy 361 gaaattaacctgaatggaacatgcctaaaggaccatccagccaaatgttcatattat 420
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Db 261 GAAATTAACCTGAATGGAACATGCCTAAAGAGCCCATTCAGGCCAAATGTTTCATTTAT 202
Qy 421 gaaattgaattcacagagatgggtactacttgggtgactaccacacagttgagaatgagata 480
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Db 201 GAAATGGAATTCACAGAGGATGGTACTACTTGGGTGACTACCACAGTTGAGAATGAGATA 142
Qy 481 caaatcacagaacatcaaatgaaagccaaataattatgcttttggtaagaagtaaaagt 540
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Db 141 CAAATCAAGAACAATCAAAATGAAAGCCAAATAATTATGCTTTTGGTAAGAAGTAAAGTG 82
Qy 541 aaattatttctcagatgatggaatctggagtgagtgagtgatgatacaaatgctggaaa 600
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Db 81 AATATTTATTGCTCAGATGATGGAATCTGGAGTGGAGTGAGTGAGTGAACAATGCTGGAAA 22
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Db 21 GGTGATATCTGGAAGAAACC 1

RESULT 12
AX280336 AX280336 1686 bp DNA linear PAT 02-NOV-2001
LOCUS
DEFINITION Sequence 71 from Patent WO0177332.
ACCESSION AX280336
VERSION AX280336.1 GI:16607714
KEYWORDS
SOURCE
dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 71 18-OCT-2001;
Heska Corporation (US)
FEATURES
Location/Qualifiers
source 1..1686
/organism="Canis familiaris"
/db_xref="taxon:9615"
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/note="unnamed protein product"
/codon_start=1
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/db_xref="GI:16607715"
/translaton="MSLSNAEIKVNPDPQDFEIVDPGYLGLYLSLOWQPPLEPNFKEC
TIYELKRYNIDSENWKIITKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRSM
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AECTDYIKVANGKNGCRFPYLESSDYKDFIVCEIYEIETEDGTWTWTTVNEIOITPT
PPDYLSUTVKNSEINLKNWPKPIPAKCFIVEIETEDGTWTWTTVNEIOITPT
SNESOKLCFLVRKSNLYICSDGKISWSESDQCKGDIWKETGSNTKVDKPVNECRPC
TDPPCPVPEPLGGPSVLIPPPKDLIRITRPEVTCVVDLGLREDPEVQISWFDVG
KEVHTAKTSREQFNCTYRVSVLP IEHQDMLTGKREKRVKNHIDLPSPIERTISKA
KGRAHKPSVYVLPSPKELSSSDTSITCLIKDFYPPDIDVWQSNQGOQPEPKRHMT
PPQIDEDGSYFLXSKLSVDKSRWQQGDPFTCAVMHETLQNHITDLSLSHSPGK"
BASE COUNT 513 a 384 c 382 g 407 t
ORIGIN
Query Match 70.4%; Score 617.8; DB 6; Length 1686;
Best Local Similarity 99.7%; Pred. No. 1.6e-114;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caaggaaatcggaactaaattcaagatatgactgtgtatatcaaacctggcaatat 60
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Db 334 CAAGGAAATCGGAAACTAAAATTAAGATATGAGTGTGTATATTAACAACTGCAATAT 393
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Qy	61	ttagctctgctcttggaacctggacatgggtgtccattttgtatcacaattaccagttgttt	120
Db	394	TTAGTCTGCTCTTTGGAAACCTGGCATGGGTGTCCATTTTGATACCAAAATPACCAGTTGTTT	453
Qy	121	tactggatagaggcgcttgaccattcagacagatgtactgattacatcaagtttaatgga	180
Db	454	TACTGGTATGAGGGCTTGGACCAATTGAGCAGAGTGTACTGTTTACATCAAGGTTTAATGGA	513
Qy	181	aaaaatatggatgacaggtttccctatttggagtcacagacataaaagattctcacatc	240
Db	514	AAAAATATGGATGTCAGGTTTCCTATTTTGGAGTCATCAGACTATAAGATTTCCTACATC	573
Qy	241	tgtgttaatgggtcatcagaatcccagcgcctatcagaccagctattttatttttcagott	300
Db	574	TGTGTTAATGGGTATCAGAAATCCCAGCCTATCAGACCCAGCTATTTTATTTTTCAGCTT	633
Qy	301	caaaatatgtataaacctatgcccacagactacctagttcttactgtgaagaattcagag	360
Db	634	CAAAATATAGTTTAAACCTATGCCACCAGACTACCTTTAGTCTTACTGTGAAGAAATTCAGAG	693
Qy	361	gaaattaacctgaaatggaacatgcctaaggaccattccagccaaaatggttccatttat	420
Db	694	GAAATTAACTGAAATGGAAATGCGCTTAAGGACCCATTCCAGCCAAATGTTTTCATTAT	753
Qy	421	gaaattgaattcacagagatggtactacttgggtgactaccacagtttgagaatcagata	480
Db	754	GAAATTGAATTCACAGAGGATGGTACTACTTGGGTGACTTACCACAGTTGAGAAATGAGATA	813
Qy	481	caaatcacagaacatcaaatgaaagccaaaaattatgctttttggtaagaagtaagtg	540
Db	814	CAAAATCACAGAACATCAATGAAAGCCAAAAAATATGCTTTTGGTAGAAGCTAAAGTG	873
Qy	541	aatattattgctcagatgatggaatctctggagtggagtggatgagaacaatctctggaaa	600
Db	874	AATATTTTATTGCTCAGATGATGGAATCTCGAGTGTAGTGGAGTGATGAACAATGCTGGAAA	933
Qy	601	ggtgacatatggaaggaacc	621
Db	934	GGTGATATCTGGGAAGGAACCC	954

RESULT 13
AX280338/c LOCUS linear DNA 1686 bp PAT 02-NOV-2001
Sequence 73 from Patent WO0177332.
AX280338 ACCESSION
AX280338.1 GI:16607716
. VERSION
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13 receptors
JOURNAL Patent: WO 0177332-A 73 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
source 1..1686
/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 407 a 382 c 384 g 513 t
ORIGIN

Query Match 70.4%; Score 617.8; DB 6; Length 1686;
Best Local Similarity 99.7%; Pred No. 1 6e-114;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 caaggaaatcggggaactaaaaattcaagatatgtgacctgttatattacaactggcaatat 60
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Dd	1353	CAGGAATCGGGAAACTAAAATTCAAGATATGACGTGCTATATTTACAACCTGCCAATAT	1294
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Dd	1293	TTAGTCTGCTCTTGGAACCTGGCATGGGTGCCATTTTGATACCAATTAACCAAGTTGTTT	1234
Qy	121	tacttggatatagggtcttggaccatttcagacagagtgtactgttacatcaaggttaataaga	180
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Dd	813	AATATTATTTCCTCAGATGATGGAATCTGGNGTGGTGGAGTGATGAACAATGCTGGAAA	754
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RESULT 14
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LOCUS
DEFINITION 1686 bp DNA linear PAT 02-NOV-2001
ACCESSION Sequence 80 from Patent WO0177332.
VERSION AX280345
KEYWORDS 1 GI:16607723
SOURCE
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (sites)
Mcall,C.A. and Tang,L.
Compositions and methods related to canine igg and canine il-13
receptors
Patent: WO 0177332-A 80 18-OCT-2001;
Heska Corporation (US)
Location/Qualifiers
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1. .1686
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BASE COUNT 512 a 388 c 379 g 407 t
ORIGIN

Query Match 70.4%; Score 617.8; DB 6; Length 1686;
Best Local Similarity 99.7%; Pred. No. 1.6e-114;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 934 GGTGATATCTGGAAGGAAC 954

RESULT 15
AX280347/c
LOCUS AX280347 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 82 from Patent WO0177332.
ACCESSION AX280347
VERSION AX280347.1 GI:16607725
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (sites)
REFERENCE 1 Mccall,C.A. and Tang,L.
*AUTHORS Compositions and methods related to canine igg and canine il-13
*TITLE

receptors
Patent: WO 0177332-A 82 18-OCT-2001;
Heska Corporation (US)
FEATURES Location/Qualifiers
source 1..1686
/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 407 a 379 c 388 g 512 t
ORIGIN

Query Match 70.4%; Score 617.8; DB 6; Length 1686;
Best Local Similarity 99.7%; Pred. No. 1.6e-114;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 caaggaatcggaactcaaatcaagatgagctgtgtatatacaactggcaatat 60
Db 1353 CAAGGAATCGGAAACTTAAATTCAGATATGGACTGTGTATATACAACTGGCAATAT 1294
Qy 61 ttagtctgtcttggaaacctggatgggtgtccattttgtataccaatcaccagttgttt 120
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Qy 241 tgtgttaattgggtcatcagaatcccgacctatcagaccagctatttttttttcagctt 300
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Qy 481 caaatcaagaagaacatcaaatgaaagccaaataattatgctttttgttaagaagtaaatg 540
Db 873 CAAATCAAGAAGAACATCAAAATGAAAGCCAAATTTATGCTTTTGGTAAGAAGTAAAGTG 814
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Db 753 GGTGATATCTGGAAGGAAC 733

Search completed: September 23, 2002, 15:11:35
Job time: 13188 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:51:06 ; Search time 14.67 seconds
(without alignments)
642.691 Million cell updates/sec

Title: US-09-828-995B-61

Perfect score: 2132

Sequence: 1 MAFIHLVDGFLYLLVCTAF.....LLKTIPTKKEVFSHQDTFC 386

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1503	70.5	380	4	US-08-846-340-4
4	1503	70.5	380	4	US-08-846-344-4
5	1271.5	59.6	383	1	US-08-609-572-2
6	1271.5	59.6	383	4	US-08-841-751-2
7	1271.5	59.6	383	4	US-08-846-340-2
8	1271.5	59.6	383	4	US-08-846-344-2
9	318.5	14.9	427	4	US-08-969-125-9
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ALIGNMENTS

RESULT 1
US-08-609-572-4
: Sequence 4, Application US/08609572
: Patent No. 5710023
: GENERAL INFORMATION:
: APPLICANT: Collins, Mary
: APPLICANT: Donaldson, Debra
: APPLICANT: Fitz, Lori
: APPLICANT: Neben, Tamlyn
: APPLICANT: Whittiers, Matthew
: APPLICANT: Wood, Clive
: TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: MA
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/609,572
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: REFERENCE/DOCKET NUMBER: G15268
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 380 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-609-572-4

Query Match 70.5%; Score 1503; DB 1; Length 380;
Best Local Similarity 72.9%; Pred No. 2,4e-138;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

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RESULT 2
US-08-841-751-4
; Sequence 4, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/841.751
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-841-751-4
Query Match 70.5%; Score 1503; DB 4; Length 380;
Best Local Similarity 72.9%; Pred. No. 2.4e-138;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;
QY 1 MAFIHLVDGYLTVLAVCTAFG-SMLSNAEIKVNPDPQDFEIVDPGYLGLYLQWQPLPFD 59
Db 1 MAFVCLAIAGCLYTLFLISTFGCTSSSDTEIKVNPDPQDFEIVDPGYLGLYLQWQPLSLD 60
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RESULT 3
US-08-846-340-4
; Sequence 4, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/846.340
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-340-4

Query Match 70.5%; Score 1503; DB 4; Length 380;
Best Local Similarity 72.9%; Pred. No. 2.4e-138;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

QY 1 MAFTHLDVGFYTLVCTAFG-SMLSNAEIKVNPQDFEIVDPGVLGYSLOWQPPPLPD 59
DB 1 MAFVCLAIGCLYTLISTTFCGCTSSSTEIKVNPQDFEIVDPGVLGYSLOWQPPPLSLD 60
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DB 241 PVYLTFRESSCEIKLWSIPLGPIPARCFDYEIREDDTTLVTATVENETYLKTTNE 300
QY 300 SOKLCFLVRKVNICYSDDGIIWSEWSDQCKWG-DINKETLVFLIPAFVSIYVITC 358
DB 301 TRQLCFVVRKVNICYSDDGIIWSEWSDQCKWEGEDLSKTLLEWLPFGFILLIVFVTG 360
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DB 361 LLLRKPNTPYKMI 373

RESULT 4

US-08-846-344-4
Sequence 4, Application US/08846344
Patent No. 6258480
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,344
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-846-344-4

Query Match 70.5%; Score 1503; DB 4; Length 380;
Best Local Similarity 72.9%; Pred. No. 2.4e-138;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

QY 1 MAFTHLDVGFYTLVCTAFG-SMLSNAEIKVNPQDFEIVDPGVLGYSLOWQPPPLPD 59
DB 1 MAFVCLAIGCLYTLISTTFCGCTSSSTEIKVNPQDFEIVDPGVLGYSLOWQPPPLSLD 60
QY 60 NFKECTIEYELKYNIDSENKTKITIKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVR 119
DB 61 HFKECTVEYELKYNIGSETWKTITIKNLHYKDGFDLNGKIEAKIHTLLPWQCTNGSEVQ 120
QY 120 SSWAETTYWSPQGNRETKIQDMDCVYNNWQYLVCSPKPGVGHFDNYQLFYWYEGLDH 179
DB 121 SSWAETTYWSPQIGIPETKVQDMDCVYNNWQYLVCSPKPGVGLDNTNLYNLFYWYEGLDH 180
QY 180 SAECTDIKYNKMGCRFPYLESDDYKDFYICVNGSSEOPRPSYFIFOLQIVKPM 239
DB 181 ALQCVDIKADQNGICRFPYLEASDYKDFYICVNGSENKPIRSSYFTFOLQIVKPLP 240
QY 240 PDYLSLVTKNSEENLNKNMKGPIPAKCFYIEFTEDGTWTTVTVENEIQITRTSNE 299
DB 241 PVYLTFRESSCEIKLWSIPLGPIPARCFDYEIREDDTTLVTATVENETYLKTTNE 300
QY 300 SOKLCFLVRKVNICYSDDGIIWSEWSDQCKWG-DINKETLVFLIPAFVSIYVITC 358
DB 301 TRQLCFVVRKVNICYSDDGIIWSEWSDQCKWEGEDLSKTLLEWLPFGFILLIVFVTG 360
QY 359 LLLYKQKALLKTI 371
DB 361 LLLRKPNTPYKMI 373

RESULT 5

US-08-609-572-2
Sequence 2, Application US/08609572
Patent No. 5710023
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-572-2

Query Match 59.6%; Score 1271.5; DB 1; Length 383;
Best Local Similarity 57.2%; Pred. No. 8.9e-116;
Matches 222; Conservative 71; Mismatches 88; Indels 7; Gaps 3;
QY 1 MAFIHLVGVFLTLVCTAFGSMLSNAETKVNPPQDFEIVDPGYLGYSLQWQPLFPDN 60
Db 1 MAFVH--IRCLCFILLCTITGYSL--EIKVNPQDFEILDPGLGLYLYLQWKPPVIEK 55
QY 61 FKECTIEYELKRYNDSNWKTIITKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRS 120
Db 56 FKGCTLEYELKRYNDSNWKTIITRNLIYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQS 115
QY 121 SWAETTYTSPGNRETKIQDMDCVYNNQYLVCSWKKPGMVHFDNTYOLFVYEGLDHS 180
Db 116 PWIEASYGISDGSLETKIQDMKCIYNNQYLVCSWKKPKTVSDNTYTMFFWYEGLOHA 175
QY 181 ACCTDYIKVNGNMGRFPYLESSDYKDFYICVNGSSSQIRPSYFFIQLQNIYKPPMP 240
Db 176 LQCADYLVHDEKNVCKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTVFQLQNIYKPLPP 235
QY 241 DYLSLTVKNSSEINKLNMKPKPIPAKCFIYEIETEDGTTWVTTTVEINEIQTITSNES 300
Db 236 EFLHISVENSIDIRMKWSTPGGPPIPRCYTYEIVIREDDISWESATDKNDMLKRRANES 295
QY 301 QKLCFLVRSKVNIYCSDDGINSWSEDEQCKGDIWKETLVFFLIPIFAFVSIFVLVITCLL 360
Db 296 EDLCFFVRCKVNIYCADDGINSWSEEECEWEGYTGPDSKIIFIVPVCLEFFIFLILLCLLI 355
QY 361 LYKQALLKTIPTHT--KKEVFSHQDTFC 386
Db 356 VEKEEPEPTLSLHVDLNKEVCAYEDTLC 383

RESULT 6
US-08-841-751-2
Sequence 2, Application US/08841751
Patent No. 6214559
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive

CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/841.751
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/609,572
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-841-751-2

Query Match 59.6%; Score 1271.5; DB 4; Length 383;
Best Local Similarity 57.2%; Pred. No. 8.9e-116;
Matches 222; Conservative 71; Mismatches 88; Indels 7; Gaps 3;
QY 1 MAFIHLVGVFLTLVCTAFGSMLSNAETKVNPPQDFEIVDPGYLGYSLQWQPLFPDN 60
Db 1 MAFVH--IRCLCFILLCTITGYSL--EIKVNPQDFEILDPGLGLYLYLQWKPPVIEK 55
QY 61 FKECTIEYELKRYNDSNWKTIITKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRS 120
Db 56 FKGCTLEYELKRYNDSNWKTIITRNLIYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQS 115
QY 121 SWAETTYTSPGNRETKIQDMDCVYNNQYLVCSWKKPGMVHFDNTYOLFVYEGLDHS 180
Db 116 PWIEASYGISDGSLETKIQDMKCIYNNQYLVCSWKKPKTVSDNTYTMFFWYEGLOHA 175
QY 181 ACCTDYIKVNGNMGRFPYLESSDYKDFYICVNGSSSQIRPSYFFIQLQNIYKPPMP 240
Db 176 LQCADYLVHDEKNVCKLSNLDSSDYKDFYICVNGSSKLEPIRSSYTVFQLQNIYKPLPP 235
QY 241 DYLSLTVKNSSEINKLNMKPKPIPAKCFIYEIETEDGTTWVTTTVEINEIQTITSNES 300
Db 236 EFLHISVENSIDIRMKWSTPGGPPIPRCYTYEIVIREDDISWESATDKNDMLKRRANES 295
QY 301 QKLCFLVRSKVNIYCSDDGINSWSEDEQCKGDIWKETLVFFLIPIFAFVSIFVLVITCLL 360
Db 296 EDLCFFVRCKVNIYCADDGINSWSEEECEWEGYTGPDSKIIFIVPVCLEFFIFLILLCLLI 355
QY 361 LYKQALLKTIPTHT--KKEVFSHQDTFC 386
Db 356 VEKEEPEPTLSLHVDLNKEVCAYEDTLC 383
RESULT 7
US-08-846-340-2
Sequence 2, Application US/08846340
Patent No. 6248714
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Fitz, Lori

Query Match	59.6%	Score	1271.5;	DB	4;	Length	383;
Best Local Similarity	57.2%;	Pred.	No. 8.9e-116;				
Matches	222;	Conservative	71;	Mismatches	88;	Indels	7;
Gaps	3;						
QY	1	MAFHLDVGFLYTLTLCVATFGSMLSNAEIKVNPDPDFEIVDPDGYLGYLSLOWQPPFLPFDN	60				
DB	1	MAFVH--IRCLCFILLCTITGYSL---EIKVNPDPDFEILDGGLLYLYLOWKPPVYIEK	55				
QY	61	FKCTEYELKYRNIDSENKMTIITKNLHYKDGFDLNGKIEAKINTLLPAOCTNGSEVRS	120				
DB	56	FKGCTLEYELKYRNVDSDSKTIIITRNLIYKDGFDLNGKIEKIRTHLSECTNGSEVQS	115				
QY	121	SWAETTVWTSPOGNRETKIOMDCGVYVNWQYLVCSWKPQMGVHEDTNYQLFVWYEGLDHS	180				
DB	116	PWIEASIGIDEGSELETKIOMKCIYVNWQYLVCSWKPQTKVTSDNTNFWFVEGLDHA	175				
QY	181	AECTDYIKVNGKNGCRFPYLESSDYKDFYICVNGSSSESQPIRPSYFIQQLQNIWKMP	240				
DB	176	LOCADYLOHDEKNVGCNLSNLDSSDYKDFYICVNGSSKLEPIRSSYTFVQLQNIWKPLPP	235				
QY	241	DYLSLTVKNSEENLKNMFKGPPIPAKCFYIEIEFTEDGTTWVTTTVENETQIPTSNS	300				
DB	236	EFLHISVENSIDIRMKWSTPGGP1PPRCYTYEIVREDDISWESATDKNDMKLKRANES	295				
QY	301	QKLCFLVRKVNIIYCSDDGIWSEWSDEOCWGD1WKETLVFFLPFAFVSIVFLVITCLL	360				
DB	296	EDLCFFVRCKVNIIYACDGIWSEWSBECEWGYTGPOSKIIFIVPVCVCLFFILLLLCLLI	355				
QY	361	LYQORALLKTIFFT--KKEVFSHOOTFC	386				
DB	356	VERKEEPTTLSLHVDLNKEVCAYEDTLC	383				

Query Match	59.6%	Score	1271.5	DB 4	Length	383			
Best Local Similarity	57.2%	Pred.	No. 8.9e-116						
Matches	222	Conservative	71	Mismatches	88	Indels	7	Gaps	3

QY	1	MAETHLDVGFLYLLVCTAFCSMLSNAEIKVNPQDFEIVDPGVLGYLSLQWQPLFPDN	60
DB	1	MAFVH---IRCLCFILLCITGYSL---EIKVNPQDFEILDGGLGYLYQWKPVPVIEK	55
QY	61	FKCTEYELKYRNIDSENKTTITKLNLKOGFDLKNKTEAKINTLLPAQCTNGSEVRS	120
DB	56	FKCTEYELKYRNVDSDSKTTITRNLIIYKOGFDLKNKIEGKIRTHLSEHCTNGSEVQS	115
QY	121	SWAETTYTSPQGNRETKIQDMDCVYYNWQYLVCSWPKGMGVHFDNTYQLFYWYEGDHS	180
DB	116	PWIEASYGISDEGSLETKIQDMKCIYYNWQYLVCSWPKGKTVSDNTYTWFFWYEGDHA	175
QY	181	AECTDIKYNGKNWGRFPYLESSDYKDFICYNGSSESQPIRPSYIFQLONIIVAMP	240
DB	176	LQCADYLQHDEKYNVGCKLSLSDSDYKDFICYNGSSKLEPIRSSYTVFQLONIIVPLP	235
QY	241	DYLSLTVKNSEETNLKNWPKGPITPAKCFIYELETFDGTTWTTTWTENEIQTIRTSNES	300
DB	236	EFLHSHVENSIDIRMKWSTPGGPPIPCPYTIEIVIREDDISWESATDKMDKKLRANES	295
QY	301	QKLCFLVRKSVNYICSDDGISWSEWSDQCWKGDITWETLVFFLIPFAFVSIFVLVITCLL	360


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QY 190 NGKNMGRFP--YLESSDYKDFICVNGSSSEQIPRSPFIFOLQNIQVPMPPDYLSLTV 24
Db 190 LGRNIACWFFRTFLLSKGRDWLALVNLVNGSSKSAIRPFDQLFALHAIDQINPP--LNVT 247
QY 248 K-NSEELNKNWPKGPPIAKFCFIYIEF--TEDGTTWTTTVE-N-IQITRTSNESQKL 303
Db 248 EICTRLSIQWERKVSAPFPHCEYEVKIHNTNGVLQTEKLMNAFISII---DDLSKY 304
QY 304 CFLVRSKNVICSDDGTWSEWSDEQCQWKGDIWKETLVFFLVPFAFVSIFVLVITCLL 360
Db 305 DVQVRAAVSMCREAGLWSEWSQPIYVGNDEHREPLREWFVIVIMATICFILLISLI 361

RESULT 11
US-08-442-282-14
: Sequence 14, Application US/08442282
: Patent No. 5760204
: GENERAL INFORMATION:
: APPLICANT: Takatsu, Kiyoshi
: APPLICANT: Tominaga, Akira
: APPLICANT: Takagi, Satoshi
: APPLICANT: Murata, Yoshiyuki
: TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/442,282
: FILING DATE:
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/757,390
: FILING DATE: 10-SEP-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Misrock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 7005-030
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 8698864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 396 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-442-282-14

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	Query Match	14.7%	Score 313;	DB 1;	Length 396;
	Best Local Similarity	28.9%	Pred. No. 2.4e-22;		
	Matches 103; Conservative	62;	Mismatches 156;	Indels 36;	Gaps 15;
Qy	23	MSLSNAETKVNPPQDFEIVDPGYLGLVSLQWQPPLFPD--NFKECTIYEYELKYRNDISENWK	81		
	:	: : : : : : : : : : :	:		
Dd	22	LLPDEKISLLPVPNTIKVTG-LAQVLQLQKPNN--PDQEQRNVNLEYQVKINAPREDDDYE	78		
Qy	82	TIITKNLHYKGFDNLKNGIEAKINTLLPAQCCTNSEVRSSAAETTYTWSPOGNRTTKTD	141		
	:	: : : : : : : : : : : :	:		
Dd	79	TRIES---KCVTILHKGFSASVRTILO---NDHSLLASSASAEL-HAPGSGPTGSIVN	131		

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Qy 142 MDCVYVNWQ-----YLVCWKPGMGVHFDNTNYQLFYWYEGLDHSAECTDIK-V 189
Db 132 LTCQNTNTEDNYSLRSLQYVSLHCTWLVGTDAPEDTQYFLYIRYG--SWTECEQYSKDT 189
Qy 190 NGKNMGRCP--YLESSDYKDFYICVNGSSSESQPIRYSFIFOLQNTVPMPPDYLSLTV 247
Db 190 LGRNIACWFPTFFLSKGRGWLAVLVNGSSKHSNAIRPFDOLFALHAIQDQINPP--LNVTA 247
Qy 248 K-NSEENLNKNMKGPIPAKCFIYELEF--TEDGTTWVTTTVE--IQITRTSNESQKL 303
Db 248 EICTRLSIOEWKPSAFPHCFDYEYKIHNTNGYLOIEKLTNFAISII---DDLKY 304
Qy 304 CFLVRSKNVYCSDDGTGWSWDSBQCKWDIKWETLVFFLIPAFVSIFFVLVTCLL 360
Db 305 DVQVRAAYVSMCREAGLWSEWSQPIYVGNDEHKPLREWFVIVIMATICFLLILSLI 361

RESULT 12
US-08-442-281-14
; Sequence 14, Application US/08442281
; Patent No. 5807991
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tominaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,281
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-281-14

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	Query Match	14.7%	Score 313;	DB 1;	Length 396;
	Best Local Similarity	28.9%	Pred. No. 2.4e-22;		
	Matches 103;	Conservative 62;	Mismatches 156;	Indels 36;	Gaps 15;
QY	23	MLSNAEIKVNPQDPFEIVDPGYGLSLQWQPPFLPDP-NFKECTIETELKYRINDSENWK	81		
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
DB	22	LLPDEKISLLPPVNTFIKVTG-LAQLVLQWKPEN--PDQQRNVNLETVQKINAPKEDDYE	78		
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:

[illegible]

RESULT 13
US-08-939-727-14
; Sequence 14, Application US/08939727
; Patent No. 5916767

```

:
: GENERAL INFORMATION:
:
: APPLICANT: Takatsu, Kiyoshi
: APPLICANT: Tomimaga, Akira
: APPLICANT: Takagi, Satoshi
: APPLICANT: Murata, Yoshiyuki
: TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
: NUMBER OF SEQUENCES: 18
:

```

; ;
; CORRESPONDENCE ADDRESS;
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
;

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,7
FILING DATE:

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FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/757,390
 FILING DATE: 10-SEP-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Mirock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7005-030
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 750-9090
 TELEFAX: 212 8698864/9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-939-727-14

Query Match 14.7%; Score 313; DB 2; Length 396;
Best Local Similarity 28.9%; Pred. No. 2.4e-22;
Matches 103; Conservative 62; Mismatches 156; Indels

Matches	103	Conservative	62	Mismatches	156	Indels	36	Gaps	15
Best Local Similarity 28.9%, Fied. NO. 2.4e-22;									

[illegible]

RESULT 14

US-07-757-390-13
; Sequence 13, Application US/07757390

Patent No. 5453491
GENERAL INFORMATION:

APPLICANT: Takatsu, Kiyoshi
APPLICANT: Tominaga, Akira

APPLICANT: TOMIYAMA, AKIHIRO
; APPLICANT: Takagi, Satoshi
: APPLICANT: Murata, Yoshiyuki

APPLICANT: MUJALA, IOSHILYUK
; TITLE OF INVENTION: Human A
; NUMBER OF SEQUENCES: 19

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

;
; ADDRESS: Pennie & Edmon
; STREET: 1155 Avenue of th

```

; CITY: New York
; STATE: New York

```

COUNTRY: U.S.A.
ZIP: 10036-2711

```

;          244.10000 27.11
;          COMPUTER READABLE FORM:
;          MEDIUM TYPE: FLOPPY

```

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; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS 3.3

```

```

;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0

```

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/07/757,390

```

```

; FILING DATE: 19910910
; CLASSIFICATION: 530

```

ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-030

REFERENCE/DOCKET NUMBER: 7003-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 780-0000

TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741

```

;
;      TELEX: 66141 PENNIE
;
;      INFORMATION FOR SEQ ID NO: 13:

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; SEQUENCE CHARACTERISTICS:
;     LENGTH: 420 amino acids

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TYPE: AMINO ACID
STRANDEDNESS: unknown

TOPOLOGY: linear
MOLECULE TYPE: peptide

US-07-757-390-13

[illegible]

Query Match	14.6%	Score 3
Best Local Similarity	28.6%	Pred. N

Matches 102; Conservative 63; Mismatches 156; Indels 36; Gaps 15;

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Qy 23 MLSNAEIKVNPDPDEIVDPGVLGYLSLQWQPLPPD-NFKECTIEYELKYRNIDSENWK 81
Db 22 LLPDEKISLLPPVNFITKVKG-LAQVLLQWKPN--PDQEQRNVNLEYQVKINAPKEDDYE 78
Qy 82 TIITKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRSSWAETTYTWTSPQGNRETKIOD 141
Db 79 TRITES---KCVTILHKGFSASVRTILQ---NDHSLASSWASAEI-HAPPGSPGTSVYN 131
Qy 142 MCVVYNNQ-----YLVCSWKPGMGVHFDNYOLFVWYEGLDHSAECTDIK-V 189
Db 132 LTCITNTEDNYRSLRSQVSLHCTWLVTGDAPEDTQFLYIRYG--SWTEECQEYSKDT 189
Qy 190 NGKNMGCRFP--YLESSDYKDFIYCVNGSSSQPIRPSYFIFQLQNIKVPMPDPVLSLTV 247
Db 190 LGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSARPPDQLEFALHAIDQINPP--LNVTA 247
Qy 248 K-NSEINLKNMKGPIPAKCFIYEIEF--TEDGTTWTTTVE-N-IOITRTSNESQKL 303
Db 248 EIEGTRLSIQWEKPVSAFPIHCFDYEVIHNRNGYLQIEKLMTNAFISII---DDLKY 304
Qy 304 CFLVRSKYNIYCSDDGINSWSEDEQCKGDIWKETLVFFLIPFAFVSIFVLVITCLL 360
Db 305 DVQVRAAVSSMCREAGLWSEWSQPIYVGNDEHKPLREWFVIVIMATICIFILLISLI 361
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RESULT 15

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US-08-442-282-13
; Sequence 13, Application US/08442282
; Patent No. 5760204
; GENERAL INFORMATION:
; APPLICANT: Takatsu, Kiyoshi
; APPLICANT: Tomimaga, Akira
; APPLICANT: Takagi, Satoshi
; APPLICANT: Murata, Yoshiyuki
; TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442.282
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/757,390
; FILING DATE: 10-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7005-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 420 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-442-282-13
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Query Match 14.6%; Score 312; DB 1; Length 420;
Best Local Similarity 28.6%; Pred No. 3.3e-22;
Matches 102; Conservative 63; Mismatches 156; Indels 36; Gaps 15;
Qy 23 MLSNAEIKVNPDPDEIVDPGVLGYLSLQWQPLPPD-NFKECTIEYELKYRNIDSENWK 81
Db 22 LLPDEKISLLPPVNFITKVKG-LAQVLLQWKPN--PDQEQRNVNLEYQVKINAPKEDDYE 78
Qy 82 TIITKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRSSWAETTYTWTSPQGNRETKIOD 141
Db 79 TRITES---KCVTILHKGFSASVRTILQ---NDHSLASSWASAEI-HAPPGSPGTSVYN 131
Qy 142 MCVVYNNQ-----YLVCSWKPGMGVHFDNYOLFVWYEGLDHSAECTDIK-V 189
Db 132 LTCITNTEDNYRSLRSQVSLHCTWLVTGDAPEDTQFLYIRYG--SWTEECQEYSKDT 189
Qy 190 NGKNMGCRFP--YLESSDYKDFIYCVNGSSSQPIRPSYFIFQLQNIKVPMPDPVLSLTV 247
Db 190 LGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSARPPDQLEFALHAIDQINPP--LNVTA 247
Qy 248 K-NSEINLKNMKGPIPAKCFIYEIEF--TEDGTTWTTTVE-N-IOITRTSNESQKL 303
Db 248 EIEGTRLSIQWEKPVSAFPIHCFDYEVIHNRNGYLQIEKLMTNAFISII---DDLKY 304
Qy 304 CFLVRSKYNIYCSDDGINSWSEDEQCKGDIWKETLVFFLIPFAFVSIFVLVITCLL 360
Db 305 DVQVRAAVSSMCREAGLWSEWSQPIYVGNDEHKPLREWFVIVIMATICIFILLISLI 361
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Search completed: September 20, 2002, 11:52:40
Job time: 94 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 13:33:57 ; Search time 4150.53 seconds
(without alignments)
4728.209 Million cell updates/sec

Title: US-09-828-995B-60

Perfect score: 1454

Sequence: 1 ggcacagcgtgattgtg.....aaangaaaaaaaaaaaaa 1454

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	662.8	45.6	954	9 AL525497	AL525497 AL525497
2	641	44.1	928	9 AL562513	AL562513 AL562513
3	509.4	35.0	683	10 BG778615	BG778615 602668073
4	491.4	33.8	743	10 BG723203	BG723203 602690806
5	437.6	30.1	658	10 B1828427	B1828427 603078385
6	387.8	26.7	676	9 A1798934	A1798934 we94e04.x
7	349	24.0	926	10 BF620022	BF620022 601473366
8	346.2	23.8	715	10 BE788633	BE788633 601475992
9	320.2	22.0	445	9 AW954333	AW954333 EST366403
10	310.2	21.3	867	10 BF525412	BF525412 602069493
11	291	20.0	579	9 AW629184	AW629184 hi52b02.x
12	286.6	19.7	537	10 BF591502	BF591502 nab9a12.
13	271.2	18.7	649	10 BE289033	BE289033 601091625
14	264.4	18.2	365	9 AA298563	AA298563 EST141178
15	262.6	18.1	517	9 AW136614	AW136614 UI-H-BII-
16	261.4	18.0	476	10 BF443846	BF443846 261485 MA
17	248	17.1	379	10 BF443844	BF443844 261483 MA

c 18	233.8	16.1	506	9 AW236406	AW236406 xol59l2.x
c 19	231.4	15.9	479	9 AI358911	AI358911 qyl9c05.x
c 20	230	15.8	443	9 AA909507	AA909507 oll16dl1.s
c 21	225.6	15.5	755	10 BE619361	BE619361 601473366
c 22	223.2	15.4	675	10 BE964459	BE964459 601658166
c 23	192.4	13.2	473	10 R52795	R52795 y999f10.tl
c 24	188.2	12.9	904	10 B1462644	B1462644 603203069
c 25	185.2	12.7	396	10 BG190222	BG190222 RST9279 A
c 26	184.4	12.5	399	10 BG213456	BG213456 RST33052
c 27	180.6	12.4	403	10 BG201950	BG201950 RST21296
c 28	180.4	12.4	409	10 BG215092	BG215092 RST34750
c 29	178	12.2	360	9 AA621766	AA621766 af06dl0.s
c 30	171	11.8	823	10 BF968964	BF968964 602270160
c 31	164.6	11.3	465	10 BF523126	BF523126 UI-R-C3-s
c 32	158.2	10.9	446	9 AW001800	AW001800 ws05c01.x
c 33	150.4	10.3	465	10 R52796	R52796 y999f10.s1
c 34	128.2	8.8	341	9 AA921043	AA921043 vy75h06.r
c 35	87.4	6.0	160	9 A1547789	A1547789 UI-R-C3-s
c 36	84.8	5.8	530	12 AZ557979	AZ557979 RPCI-23-1
c 37	69.6	4.8	176	12 AZ108580	AZ108580 RPCI-23-4
c 38	58	4.0	1101	12 CNS0039G	AL063921 Drosophil
c 39	58	4.0	1201	12 CNS016E1	AL106627 Drosophil
c 40	54.2	3.7	469	12 AQ761600	AQ761600 HS_3132_B
c 41	53.2	3.7	987	12 CNS014PQ	AL104456 Drosophil
c 42	53	3.6	928	12 CNS00DKY	AL071865 Drosophil
c 43	52.8	3.6	1043	12 CNS0145P	AL103735 Drosophil
c 44	52	3.6	1101	12 CNS00EVL	AL069706 Drosophil
c 45	50.8	3.5	928	12 CNS00DKY	AL071865 Drosophil

ALIGNMENTS

RESULT 1
AL525497 954 bp mRNA linear EST 13-FEB-2001
LOCUS AL525497 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC012YF21 5
DEFINITION prime, mRNA sequence.
ACCESSION AL525497
VERSION AL525497.1 GI:12788990
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 954)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..954
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC012YF21"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com
http://fulllength.invitrogen.com"

BASE COUNT 295 a 172 c 201 g 285 t 1 others

ORIGIN

Query Match 45.6%; Score 662.8; DB 9; Length 954;
Best Local Similarity 84.0%; Pred. No. 5.3e-105;
Matches 761; Conservative 0; Mismatches 142; Indels 3; Gaps 1;

QY 150 gagtggaaacttcaaaagtattgaatcttggaggaaatggcttttcattcatttgatgtcgg 209
DB 44 GAGAGGCAATATCAAGGTTTAAATTCGGAGAAATGGCTTTTCGTTGGCTATCGG 103

QY 210 attcctctataccctgcttggtttgcacagcattggct---ctatgctttccaagtctga 266
DB 104 ATCCTTATATACCTTTCTGATAAGACACACATTTGGCTGTACTTCTTTCAGACACCGA 163

QY 267 gataaaagttaactccctccagagattttagatagtagggaccctggatattaggttatct 326
DB 164 GATAAAAGTTAACCCCTCCAGGATTTTGAGATAGTGGATCCCGGATACTTAGGTTATCT 223

QY 327 ctcttggcaatggcaacctccattatttccggataatttttaaggaatgcacaatagaata 386
DB 224 CTATTTTGCATGGCAACCCCACTGCTCTCTGGATCATTTTAAGGAATGCACAGTGAATA 283

QY 387 tgaattcaaataccgaaacattgatagtgaaacttggaagaccatcattaccagaatct 446
DB 284 TGAACCTAAATACCGAAACATTTGGTAGTGAACATGCAAGACCATCATTTACTAAGAATCT 343

QY 447 acattcaaaagtgggtttagatcttaacaaagtattgaagcaaaagataaacacattct 506
DB 344 ACATTTACAAAGATGGTGTGATCTTTAACAAAGGCATTTGAAGCCGAAGATACACACGCTTT 403

QY 507 gccagcaaatgcacaaatggatcagaagttagaagttcatggcgcaaaactacttattg 566
DB 404 ACCATGGCAATGCACAAATGGATCAGAAGTTCAAAGTTCTCTGGCGAAGAACTACTTATTC 463

QY 567 gacatcaccaacaggaatcggggaactaaaaatcgaagatgatggatgtgtattacaa 626
DB 464 GATATCACCACACAGGAATTCACAGAACTAAAGTTTCAGGATATGGATTGGCTATATACAA 523

QY 627 ctggcaatattagtcgtcttggaaacctggacatgggtgtccatttttgatacccaatta 686
DB 524 TTGGCAATATTTACTCTGTCTCTTGGAAACCTGGCATAGGTGTACTTCTTGATACCAATTA 583

QY 687 ccagttgttttactgtatgagggcttggaccatttcagcagagtgactgactgattacatcaa 746
DB 584 CAACTTGTTTTACTGTATGAGGGCTTGGATCATGCATTTACAGTGTGTTGATTACATCAA 643

QY 747 ggttaatggaaaaaatatgggtagcgaggttccctctatttggagtcacatcagactataaga 806
DB 644 GGCTGATGGACAAAATATAGGATGCGAGATTTCCCTATTTGGAGGCATCAGACTATATAAGA 703

QY 807 ttctacatctgtgttaatgggttcacagaatcccgacctatcagaccagctattttat 866
DB 704 TTTCTATATTTGTTTAAATGGATCATCAGAGAACAAGCCCTATCATGATCCAGTTATTTTCCAC 763

QY 867 ttttcagcttcaaaaatatagtttaaacctatgcacacagactaccttagttcttactgtgaa 926
DB 764 TTTTTCAGCTTCAAAATATAGTTAAACCTTTTGGCCGAGTCTATCTTACTTTTACTCGGGA 823

QY 927 gaattcaggggaaatcaactgaaatgggaacatgcctaaaggagcccatccagcccaaatg 986
DB 824 GAGTTCTATGAAATTTAAGCTGAATTTGGAGCATACCTTTTGGGACCTATTTCCAGCAAGGTG 883

QY 987 ttctatttgaattgaattcagagaggtggtactacttctgggtgactaccacagattga 1046
DB 884 TTTTGTATTTGAAATTTGAGATCAGAGAAGATGATACCTTGTGGTGCAGCTGCTACAGTTGA 943

QY 1047 gaatga 1052
DB 944 AAATGA 949

● RESULT 2

AL562513/c
LOCUS
DEFINITION
AL562513 LTI_NFL003_NBC3 Homo sapiens CDNA clone CSDDC012F21 3
prime, mRNA sequence.
ACCESSION
AL562513
VERSION
AL562513.1 GI:12911007
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 928)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .928
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 265 a 186 c 158 g 312 t 7 others
ORIGIN

Query Match 44.1%; Score 641; DB 9; Length 928;
Best Local Similarity 81.5%; Pred. No. 3.1e-101;
Matches 747; Conservative 6; Mismatches 161; Indels 3; Gaps 1;

QY 382 gaatatgaattaaaaatcacgaaacattgatagtgaaactgggaagaccatcattaccacag 441
DB 928 GGATWTGAACATAAATGACCGAAACATTTGGTAGTGACACATGGAAGACCATCATTAAG 869

QY 442 aatctacattacaagaatgggtttagctttaacaaaggatttaagaagaataaaacaca 501
DB 868 AATCTACATAACAAACATGCGTTTGATCTTTAAACAGGCATTTGAAGGAAGACACACAG 809

QY 502 ctctctcagcagaacaatgcacaaatggatcagaagtttagaagttcatggggcagaacactact 561
DB 808 CTTTTCACCATGGCAATGCACAAATGGATCAGAAGTTCAAAGTTCTCTGGCGAGAACTACT 749

QY 562 tatcgacatcacccacaagaatcgggaaactaaataattcaagatatggactgtgtatat 621
DB 748 TATTTGGATATCACACAGAAGATTCAGAAACTAAAGTTTCAGGATATGGATTGCGTATAT 689

QY 622 tacaactggcaatatttagctctctcttggaaacctggcatgggtgccatttggatacc 681
DB 688 TACAATTTGGCAATATTTTACTCTCTCTTCTGGAAACCTGGCATAGGTGTACTTCTTGATACC 629

QY 682 aattaccagttgttttactgggtatgagggcttggaccattcagcagagttgactgattac 741
DB 628 AATTACAACCTTGTTTTACTTGGTATGAGGGCTTGGATCATGCATTCACAGTGTGTGATTAC 569

QY 742 atcaaggttaattggaaaaaatatgggatgcaggtttccctatttggagtcacagactat 801
DB 568 ATCAAGGCTGATGGACAAAATATAGGATGAGATTTCCCTATTATTGGAGGCAATCAGACTAW 509

Qy 802 aaagattctacatctgtttaaagggtcacaagaatcccgacctatcagaccagctat 861
 Db 508 AAAGATWCTATAAAAAAATGAATGGATCATCAGAGACAAGCCCTATCAGATCCAGTTAT 449
 Qy 862 tttatttttcagcttcaaaataatagtttaaacctatgcccagactacacttagcttact 921
 Db 448 TTCACCTTTTCAGCTTCAAAATATAGTTAAACCTTTGGCCGAGCTATCTTACTTTTACT 389
 Qy 922 gtgaagaattcagaggaataaactgaaatggaacatgcctaaaggagccattccagcc 981
 Db 388 CGGAGAGTTCATGTGAATTAAGCTGAATGGAGCATACCTTTGGGACCTATTCACCA 329
 Qy 982 aaagtgttcatttatgaaatgaattcacagaggtgactacttctggtgactaccaca 1041
 Db 328 AGGTGTTTTGTGATTAAGAAATGAGATCAGAGAAGATGATACCTTGGTGGTACTTACA 269
 Qy 1042 gttgagaatgagatcacaaatcacagaacatcaaatgaaagccaaaataattatgttttg 1101
 Db 268 GTTGAATAAGAACATACACCTTGAAACAAACAATGAACCCGACAAATATGCTTTTGT 209
 Qy 1102 gtaagaagtaagtgaattatttctgcagatgatgaaatcctggagtgagtgatgat 1161
 Db 208 GTAAGACCAAGTGAATATTATTGCTCAGATGACGGAATTTGGAGTGAAGTGAT 149
 Qy 1162 gaacaatgctggaaggt---gacatatggaaggaacacttagtatttttcttgatacca 1218
 Db 148 AAACAATGCTGGAGGTGAAGACCTATCGAAGAAACCTTTGCTACGTTTCTGGCTACCA 89
 Qy 1219 ttgcttttgcctcaaatattgttttggtaataactgctgcttttggataaagcaagg 1278
 Db 88 TTTGGTTTCATCTTAATATAGTTATATTGTAACCGCTCTGCTTTAGCGTAAGCCAAAC 29
 Qy 1279 gcttactgaaacgat 1295
 Db 28 ACCTACCCAAAAATGAT 12

RESULT 3
 BG778615
 LOCUS 60268073F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4807603 5',
 DEFINITION mRNA sequence.
 ACCESSION BG778615
 VERSION BG778615.1 GI:14048932
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/BTP
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM1659 row: b column: 20
 High quality sequence stop: 683.
 Location/Qualifiers
 1. .683

FEATURES
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 1. .683
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4807603"
 /clone_lib="NIH_MGC_60"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (T1 phage-resistant)"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggccattatggcc
); Double-stranded cDNA was prepared from cell line RNA.
 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-ATTCTAGAGCCGAGCGCGGACATG-dt(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 Library."

BASE COUNT 212 a 124 c 140 g 207 t
 ORIGIN
 Query Match 35.0%; Score 509.4; DB 10; Length 683;
 Best Local Similarity 85.4%; Pred. No. 1.7e-78;
 Matches 580; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

Qy 161 tcaaaagtattgaattcttgaggaaatggcttcattcattcattgattcggtattcctctata 220
 Db 4 TCAAGGTTTAAATCTCGAGAAATGGCTTCGTTTGGCTATCGATCGATGCTTATATA 63
 Qy 221 cctgtctgttgcacagcatttggct---ctatgctttcaaatgctgagataaagtta 277
 Db 64 CTTTCTGATAAGCACAACTTTGGCTGTACTTCTATCTTACAGACACCGAGATAAAGTTA 123
 Qy 278 atcctcctcagatttgcagatagtgagacctggatatttagttatctctcttgcatt 337
 Db 124 ACCCTCCCTCAGATTTTGGATAGTGGATCCGGATACTTAGGTTATCTCTATTGCGAAT 183
 Qy 338 ggcaacctccattattccggataattttaaggaatgcacataagaatgatgaataat 397
 Db 184 GGCACCCCTGCTCTGGATCATTTTAAGGATGCACAGTGCAGATATGAATATAAT 243
 Qy 398 accgaacattgatagtgaaactggaagacctcattaccagaagctcattaccattacaag 457
 Db 244 ACCGAAACATTTGGTAGTGAACATGGAAGACCATCATTTACTAAGAATCTACATTACAAG 303
 Qy 458 atgggttgatcttaacaaaggtattgaagcaagaataaacaacacctctcgcagacaa 517
 Db 304 ATGGGTTTGTATCTTAACAAGGGCATTTGAAGCGAAGATACACACGCTTTTACCCTGGCAAT 363
 Qy 518 gcacaaatggatcagaagttagaagttcattggcagaaactacttattggagactcaccac 577
 Db 364 GCACAATGGATCAGAAAGTTCAAAGTCTCTGGCAGAAACTACTTATTGGATATCACAC 423
 Qy 578 aaggaaatcgaggaaactaaaaatccaagatagtgactgtgtatattacaactggcaatt 637
 Db 424 AAGGAATTCAGAAACTAAAAGTTCAGGATATGGATTGGCTATATTACAAATTTGCCAAT 483
 Qy 638 tagctgctcttgaaacctggcagtggtgtccattttgatccaactaccagttgtttt 697
 Db 484 TACTCTGTCTTGGAAACCTTGGCATAGGTGTACTTCTTGATACCAATTAACAATTTGTTT 543
 Qy 698 actggtatgaggtcttgaccattcagcagagtgactgattacatcaagggttaattgaa 757
 Db 544 ACTGTTATGAGGCTTGGATCATGCAATACAGTGTGTGATTACATCAAGGCTGATGAC 603
 Qy 758 aaaaatggatgcaggtttccctatttggagctcagactataaagatttctacatct 817
 Db 604 AAAATATAGGATGCAGATTTCCCTATTTGGAGGCATCAGACTATAAAGATTCTTATATT 663
 Qy 818 gtgttaaatgggtcatcaga 836
 Db 664 GTGGTACTGGATCATCAGA 682

RESULT 4
 BG723203
 LOCUS
 DEFINITION 602690806F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4823185 5',
 linear EST 08-MAY-2001

```

mRNA sequence.
ACCESSION BG723203
VERSION BG723203.1 GI:14002390
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 743)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10732 row: 1 column: 02
High quality sequence stop: 730.
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            /clone_lib="NIH_MGC_97"
            /lab_host="DH10B"
            /note="Organ: testis; Vector: pBluescriptR (modified
            pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcag
            ); Oligo-dT primed using primer 5'-tttttttttttttttVN-3',
            size-selected for average insert size 2.2 kb and
            normalized to 10^5. This is a primary library enriched
            for full-length clones and constructed using the
            Cap-trapper method (Carninci, in preparation). Library
            constructed by M. Brownstein (NIMH/NHGRI, National
            Institutes of Health). Note: this is a NIH_MGC Library."
        229 a 135 c 164 g 214 t 1 others
BASE COUNT 229 a 135 c 164 g 214 t
ORIGIN
Query Match 33.8%; Score 491.4; DB 10; Length 743;
Best Local Similarity 84.5%; Pred. No. 2 le-75;
Matches 576; Conservative 0; Mismatches 102; Indels 4; Gaps 2;

QY 150 gagtggaaacttcaagattgaattgttgagggaattgggttcattcatttggtgctgg 209
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 49 GAGAGGCAATATCAGGTTTAAATCTCGAGAAATGGCTTTCGTTGCTATCGG 108

QY 210 attctctataccctgtctgtttgcacacacatttggtct---ctatgctttcaaatgctga 266
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 109 ATGCTTATATACCTTCTGATAGACACACATTTGGCTGTACTTTCATCTTCAGACACCGA 168

QY 267 gataaaagttaattccctccaggattttgagatagtgagccctgagatttttaggttatct 326
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 169 GATAAAGTTAACCTCTCCACAGA-TTTCAGATAGTGGATCCCGGATCTAGTTATCT 227

QY 327 ctcttgcgaatggaacccctccatttattccgcgataattttaagggaatgcacaaagaata 386
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 CTATTGGCAATGGCAACCCCACTGCTCTGGATCATCTTTAAGGAATGCACAGTGAATA 287

QY 387 tgaattaaataaccgaaacattgtagtgaacactggaagaccatcattaccagaatct 446
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 288 TGAACATAAATACCGAAACATTTGGTAGTGAACATGGAAGACCATCATCTACTAAGAATCT 347

QY 447 acctataaagatgggtttgattcttaacaaaggattgaagcaaaagataaacaactctct 506
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 348 ACATTACAAGATGGGTTCATCTTAACAAGGGCATTTGAAGCGAAGATACACACGCTTTT 407

QY 507 gccagcacaatgcacaaatggtatcagaagttgaagttcatgtggcgagaactactatttg 566
```

```

||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 408 ACCATGGCAATGCACAAATGGATCAGAACTTCAAAGTCTCTGGCGAGAACTACTTATNG 467
QY 567 gacatcacacaaggaaaatcgggaaaactaaaattcaagatatgagctgtgtattacaa 626
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 468 GATATCACCACAAAGGAATTCACAGAACTAAAGTTACAGGATATGGATTGGGTATATTACAA 527
QY 627 ctgggcaatttagtctgctctcttggaacctgagcatgggtgccatttgataccaattta 686
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 528 TTGGCAATATTACTCTGTCTTGGAAACCTGGCATAGGTACTTCTTGATACCAATTA 587
QY 687 ccagttgttttactggtgatgggcttgaccattcagcagagtgactgattacatcaa 746
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 588 CAACCTGTTTACTGCTATGAGGCTTGGATCATGATCATACAGTGTGTTGATTACATCAA 647
QY 747 ggttaattgaaaaataatcggatcgaggttccctcatttggagtcacagcattataaaga 806
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 648 GGCTGATGACAAAATATAGGATGCAGATTTCCCTAATTGGAGGCATCAGACTATAAGA 707
QY 807 ttctacatctgtgtaattggg 828
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Db 708 TTCTATATTGTTGTTAATGG 729

RESULT 5
LOCUS BI828427
DEFINITION 603078385F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5170268 5',
mRNA sequence.
ACCESSION BI828427
VERSION BI828427
KEYWORDS EST.
SOURCE BI828427.1 GI:15939977
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 658)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11423 row: 1 column: 21
High quality sequence stop: 651.
FEATURES
    Location/Qualifiers
        1..658
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:5170268"
            /clone_lib="NIH_MGC_119"
            /tissue_type="medulla"
            /lab_host="DH10B"
            /note="Organ: brain; Vector: pCMV-Sport6; Site.1: NotI;
            Site.2: EcoRV (destroyed); RNA source normal medulla from
            anonymous male age 27. Library is oligo-dT primed and
            directionally cloned (EcoRV site is destroyed upon
            cloning). Average insert size 1.3 kb, insert size range
            0.9-3 kb. Library is normalized and enriched for
            full-length clones and was constructed by C. Gruber
            (Invitrogen). Research Genetics tracking code 013. Note:
            this is a NIH_MGC Library."
        202 a 121 c 141 g 194 t
BASE COUNT 202 a 121 c 141 g 194 t
ORIGIN
Query Match 30.1%; Score 437.6; DB 10; Length 658;
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Query Match 23.8%; Score 346.2; DB 10; Length 715;
Best Local Similarity 77.5%; Pred. No. 2.4e-50;
Matches 526; Conservative 0; Mismatches 133; Indels 20; Gaps 8;

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Qy 394 aaataccgaacattgtagtgaacactggaagaccatcatcacaagaattctacattac 453
Db 5 AAATACCGAACAATGGTAGTGAACATGGGAAGACCATCATCTACTAAGAATCTACATTAC 64
Qy 454 aaagatgggtttgattcttaacaaaggattatgaagcaagaataaacacacacttctgccc 510
Db 65 AAAGATGGGTTTGATCTTTAAACAGGGCATTGAAGCGAAGATACACACGCCCTTTACCTAT 124
Qy 511 gcaaatgcacaaatggatca----gaagttagaagtctatggcgagaactacttattg 566
Db 125 GCGCAATGGGCACAACTGGCATCAGCAAGTTTCAAAGTTTCCCTGGCGAGAACTACTTATTG 184
Qy 567 gacatcaccacaaagaatcggaactaaactaaactcaagatgactgtgtatatcaaa 626
Db 185 GATATCACCACAGAAATTCAGAAACTTAAAGTTTCAGATATGGAATTCGGTATATACAA 244
Qy 627 ctggcaatatttagctctgtcttggaaacctggcatgggtgtccattttgtataccaatta 686
Db 245 TTGGCAATATTACTCTCTTCTGGAAACCTGGCATAGGTGACTTCTTGATACCAATTA 304
Qy 687 ccagttgttttactggtgatgagggcttggaccattcagcagagtgactgattacaata 746
Db 305 CAACCTTGTGTTTACTGGTATGAGGGCTTGGATCATGCAATTCAGTGTGCGATTACATCA 364
Qy 747 ggttaatgaaaaaataatgagatcgaggtttccctatttggatgactcagactata-aag 805
Db 365 GGCTGATGGACAAAATATAGGATCGAGATTTCCTTATTTGGAGGCATCAGACTATACAA 424
Qy 806 atttctaca----tctgtttaatgggtcatcagaatcccagcctatcagaccagctat 861
Db 425 ATTCTATACTTGTCTGTTACACTGGATCATCAGAGAACAAGCCTATCAGATCCAGTTAT 484
Qy 862 tt-tattttcagcttcaaaa--atattagttaaacctatgcccacagacactccttagct 917
Db 485 TTCCACTTTTTCAGCTTCAACATATACGCTTAAACCTATGCGCGAGCTATCTTACTTATTA 544
Qy 918 tactgtgaagaattcagaggaaaattaaacctgaattggaactgcttaaaagga---cccat 974
Db 545 AACTCGGAGAGTTCATGTGAAATTAAGCTGACATGGGAGGATACCTACCGAGAGACCTAT 604
Qy 975 tccagcgaattgttctatttgaattgaattcagacagatggtactacttgggtg-a 1033
Db 605 CCACCCAGGTGCTACCGATCATGACATTCGGATCAGAGAAGATGATATACCTCGGTGAA 664
Qy 1034 ctaccacagttgagaatga 1052
Db 665 CTGCTACAGTCGAAAATGA 683
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RESULT 9
AW954333 445 bp mRNA linear EST 01-JUN-2000
LOCUS EST366403 MAGE resequences, MAGC Homo sapiens cDNA, mRNA sequence.
ACCESSION AW954333
VERSION AW954333.1 GI:8144016
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 445)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspar,R., Gay,C., Holt
I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.

TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 62

Seq primer: Reverse.
Location/Qualifiers
1. .445

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGC"
/note="vector: paluescriptSkM"

BASE COUNT 137 a 77 c 88 g 143 t
ORIGIN

Query Match 22.0%; Score 320.2; DB 9; Length 445;
Best Local Similarity 82.5%; Pred. No. 8.7e-46;
Matches 367; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

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Qy 630 gcaatatttagctcttggaaacctggcatgggtgtccattttgtataccaataacca 689
Db 1 GCAATATTACTCTCTTCTTGGAAACCTGGCATAGGTGACTTCTTGATACCAATTACAA 60
Qy 690 gttgttttactggtgatgagggcttggaccattcagcagagtgactgattacaatggt 749
Db 61 CTTGTTTTTACTGGTATGAGGGCTTGGATCATGCAATTCAGTGTGTTGATTACATCAAGGC 120
Qy 750 taatgaaaaaataatgagatcgaggtttccctatttggatgactcagactataaagattt 809
Db 121 TCATGGACAAAATATAGGATCGAGATTTCCTTATTTGGAGGCATCAGACTATAAAGATT 180
Qy 810 ctacatctgtttaatgggtcatcagaatcccagcctatcagaccagactattttatttt 869
Db 181 CTATATTGTTGTTAATGGATCATCAGAGAACAAGCCTATCAGATCCAGTTATTTCACTTT 240
Qy 870 tcagcttcaaaaatagtttaaacctatgcccacagactacaccttagcttactgtgaaaga 929
Db 241 TCAGCTTCAAAATATAGTTAAACCTTTGCGCGCAGCTATCTTACTTTTACTCGGGAGAG 300
Qy 930 ttcagaggaataatccctgaaatggaacatgctctaaaggaccattccagcgaatggttt 989
Db 301 TTCTATGTGAATTAAGCTGAATGGAGGATACCTTTTGGACCTATTTCACGCAAGGTGTTT 360
Qy 990 catttatgaattgaattcagagagtggtactacttgggtgactacacagttgagaa 1049
Db 361 TGATTATGAATTTGAGATCAGAGAAGATGATACTACCTTGGTGACTGCTACAGTTGAANA 420
Qy 1050 tgagatacaaatcacaagaacatca 1074
Db 421 TGAACATACACCTTTGAAAACAACA 445
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RESULT 10
BF525412 867 bp mRNA linear EST 11-DEC-2000
LOCUS BF525412
DEFINITION 602069493F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4212574
ACCESSION 5', mRNA sequence.
VERSION BF525412
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 867)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.


```

Db 279 AGTGAGTGGAGTGATAACAATGCTGGGAAGTGAAGACCTATCGAAGAAACTTTTGCTA 220
Qy 1204 tttttctgataccattgcttctgctcaaatattgttttggttaataacttgcctgctt 1263
Db 219 CGTTTCTGGCTACCAATTTGGTTTCATCTAATATTAGTTATATTGTAAACCGGCTGCTT 160
Qy 1264 ttgtataagcaaaaggcttctactgaaacagat-----ctttcatacaaaaaaagaagt 1316
Db 159 TTGGCTAAGCCAAACACCTACCCAAAATGATTCGACGAATTTTCTGTGATACATGAAGA 100
Qy 1317 cttttctcatacaaacacattcttgactcagtaaacctttcagctcttatgcccagatgtt 1376
Db 99 CTTTCCATATCAAGAGACATGGTATTGACTCAACAGTTTCCAGTC--ATGGCCAAATGTT 42
Qy 1377 aaatatgagctttattataaactgaagcttt 1405
Db 41 CAATATAAATCTCCATAAACTGAATTTTT 13

RESULT 12
LOCUS BF591502/c
DEFINITION nab99a12.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3275807 3'
Similar to SW:1132_HUMAN Q14627 INTERLEUKIN-13 RECEPTOR ALPHA-2
CHAIN PRECURSOR ;, mRNA sequence.
ACCESSION BF591502
VERSION BF591502.1 GI:11683826
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 537)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 480.
Location/Qualifiers
1. 537
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3275807"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTCGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 161 a 108 c 94 g 170 t 4 others
ORIGIN
Query Match 19.7%; Score 286.6; DB 10; Length 537;
Best Local Similarity 74.8%; Pred. No. 5.2e-40;

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Matches 400; Conservative 0; Mismatches 123; Indels 12; Gaps 3;
Qy 883 atagttaaacctatgccaccagactaccttagcttactgtgaagaattcagagaaatt 942
Db 537 ATAGTTAAACCTTTGCCGCCAGTCTATCTTACTTTACTCGGAGAGTTCATGTGAATTT 478
Qy 943 aacctgaatggaacatgcctaaaggccccaccatcagcccaaatgtttcattatgaaatt 1002
Db 477 AAGCTGNAATGAGCANACCTTTGGGACCTATTTCAGCAAGGTGTTTGTATTATGAATTT 418
Qy 1003 gaattcacagaggttggtactcttggtgactaccagttgagaatgagatacaaatc 1062
Db 417 GAGATCAGAGAAGATGATACCTTGGTGCTGCTAGTTGAAAATGAAACAGACACC 358
Qy 1063 acaagaacatcaaatgaaagccaaaattatgcttttggtaagaagtaaaagtgaattt 1122
Db 357 TTGAAAACAACAATGAAACCGACAAATATGCTTTGTAGTAAGAAGCAAAAGTGAATATT 298
Qy 1123 tattgctcagatgatggaatctctgagtgagtgagtgagtgagtgagtgagtgagtgagtg 1179
Db 297 TATTGCTCAGATGACGGAATTTGGAGTGAGTGGAGTGATGATGATGATGATGATGATGAT 238
Qy 1180 gacatatgaaagaaaccttagtatttttcttgataccattgttcttctcacaattt 1239
Db 237 GACCTATCGAAGAAACCTTTGCTACGTTTCTGGCTACCATTTGGTTTTCATCTTAATATT 178
Qy 1240 gtttttgtaataaacttgctgcttttctgataagcaaaaggcttttactgaaaacgat---- 1295
Db 177 GTTATATTGTAAACCGGCTGCTTTGGGTAAAGCAACACCTACCCAAAATGATTCCTCA 118
Qy 1296 ---ctttcatacaaaaaagaagctcttttctctcaatcaagacacattctgttactcagtaa 1352
Db 117 GAATTTTCTGTGANACATGAAGACTTTCATATATCAAGAGACATGTTATGTTACTCAACAG 58
Qy 1353 ctttcagctctatgccagatgttaaatatgagctcttataaactgaagcttttc 1407
Db 57 TTTCCAGTC--ATGGCCAAATGTTCAATATGATGCTCTCAATAAACTGAATTTTTC 5

RESULT 13
LOCUS BE289033
DEFINITION 601091625F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3486223 5',
mRNA sequence.
ACCESSION BE289033
VERSION BE289033.1 GI:9169136
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 649)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM8522 row: a column: 08
High quality sequence stop: 513.
Location/Qualifiers
1. 649
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone="IMAGE:3486223"
/clone_lib="NCI_CGAP_Mam5"
FEATURES
source

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:52:21 ; Search time 13.4 Seconds
(without alignments)
1115.354 Million cell updates/sec

Title: US-09-828-995B-61
Perfect score: 2132
Sequence: 1 MAFIHLVGVFLYLLVCTAF.....LLKTIPTKKEVFSHQDTFC 386

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match %	Length DB	Description
1	1503	70.5	380	1 I132_HUMAN Q14627 homo sapien
2	346	16.2	424	1 I131_MOUSE Q09030 mus musculus
3	318.5	14.9	427	1 I131_HUMAN P78552 homo sapien
4	313	14.7	420	1 I15R_HUMAN Q01344 homo sapien
5	266	12.5	415	1 I15R_MOUSE P21183 mus musculus
6	256	12.0	831	1 PRLR_CHICK Q04594 gallus gall
7	240.5	11.3	831	1 PRLR_MELGA Q91094 meleagris g
8	232	10.9	369	1 CYRG_HUMAN P31785 homo sapien
9	221	10.4	878	1 I13B_MOUSE P26954 mus musculus
10	221	10.4	896	1 CYRB_MOUSE P26955 mus musculus
11	217.5	10.2	830	1 PRLR_COLLI Q90374 columba liv
12	216	10.1	373	1 CYRG_CANFA P40321 canis famil
13	208	9.8	369	1 CYRG_MOUSE P34902 mus musculus
14	199	9.3	379	1 CYRG_HUMAN Q95118 bos taurus
15	195	9.1	581	1 PRLR_BOVIN Q28172 bos taurus
16	194	9.1	610	1 PRLR_RAT P05710 rattus norv
17	192	9.0	897	1 CYRB_HUMAN P32927 homo sapien
18	189	8.9	608	1 PRLR_MOUSE Q08501 mus musculus
19	182.5	8.6	581	1 PRLR_CEREL Q28235 cervus elap
20	180.5	8.5	630	1 PRLR_ORENI Q91513 oreochromis
21	178	8.3	616	1 PRLR_RABIT P14787 oryctolagus
22	172.5	8.1	622	1 PRLR_HUMAN P16471 homo sapien
23	154.5	7.2	917	1 I16B_MOUSE Q00560 mus musculus
24	150	7.0	918	1 I16B_HUMAN P40189 homo sapien
25	145	6.8	918	1 I16B_RAT P40190 rattus norv
26	144.5	6.8	400	1 GNCR_HUMAN P15509 homo sapien
27	139	6.5	862	1 I12S_HUMAN Q99665 homo sapien
28	136.5	6.4	638	1 GHR_PIG P19756 sus scrofa
29	131.5	6.2	378	1 I13R_HUMAN P36951 homo sapien
30	129	6.1	1282	1 DOME_DROME Q9VWE0 drosophila
31	127.5	6.0	638	1 GHR_RABIT P19941 oryctolagus
32	127.5	6.0	1630	1 PTP1_DROME P35992 drosophila
33	126	5.9	611	1 GHR_COLLI Q90375 columba liv

ALIGNMENTS				
RESULT 1				
ID	I132_HUMAN	STANDARD;	PRT;	380 AA.
AC	Q14627; Q00667;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Interleukin-13 receptor alpha-2 chain precursor (Interleukin-13 binding protein).			
GN	IL13RA2 OR IL13R.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUP-Renal cell carcinoma;			
RA	MEDLINE=96279273; PubMed=8663118;			
RA	Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N., Ferrara P.;			
RA	"Cloning and characterization of a specific interleukin (IL)-13 binding protein structurally related to the IL-5 receptor alpha chain.";			
RL	J. Biol. Chem. 271:16921-16926(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUP-Testis;			
RA	Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H., Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;			
RA	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUP-Brain;			
RA	MEDLINE=97321053; PubMed=9177784;			
RA	Guo J., Apiau F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.;			
RT	"Chromosome mapping and expression of the human interleukin-13 receptor.";			
RL	Genomics 42:141-145(1997).			
CC	-1- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13 (IL-13), BUT NOT TO IL-4.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
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CC	-----			
DR	EMBL; X95302; CAA64617.1; -;			
DR	EMBL; U70981; AAB17170.1; -;			
DR	EMBL; Y08768; CAA70021.1; -;			
DR	MIN; 300130; -;			

34	126	5.9	1165	1	LEPR_HUMAN	P48357 homo sapien
35	124.5	5.8	1097	1	LIFR_HUMAN	P42702 homo sapien
36	124	5.8	825	1	IL4R_HUMAN	P24394 homo sapien
37	121.5	5.7	608	1	GHR_CHICK	Q02092 gallus gall
38	119.5	5.6	638	1	GHR_HUMAN	P10912 homo sapien
39	118	5.5	650	1	GHR_MOUSE	P16882 mus musculus
40	117.5	5.5	634	1	GHR_SHEEP	Q28575 ovis aries
41	117	5.5	327	1	I12B_CEREL	Q28234 cervus elap
42	116.5	5.5	634	1	GHR_BOVIN	P79108 bos taurus
43	116	5.4	507	1	EPOR_RAT	Q07303 rattus norv
44	115	5.4	329	1	I12B_HORSE	Q9XS05 equus cabal
45	114	5.3	507	1	EPOR_MOUSE	P14753 mus musculus

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DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003532; Hematopo_receptor_S_F2.
DR Pfam: PF00041; fn3; 1.
DR PROSITE: PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 380
FT DOMAIN 27 343
FT TRANSMEM 344 363
FT DOMAIN 364 380
FT DISULFID 145 155
FT CARBOHYD 115 197
FT CARBOHYD 215 215
FT CARBOHYD 290 290
FT CARBOHYD 299 299
SQ SEQUENCE 380 AA; 44176 MW; 3C6ACB1B5562C887 CRC64;

Query Match 70.5%; Score 1503; DB 1; Length 380;
Best Local Similarity 72.9%; Pred. No. 1.6e-118;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

QY 1 MAFIHLVDGFLYLLVCTAFG-SMLSNAEIKVNPQDFEIVDYGVLGVLQWQPPLEPD 59
DB 1 MAFVCLAIAGCLYELISTEFGCTSSSDTEIKVNPQDFEIVDYGVLGVLQWQPPLEPD 60

QY 60 NPEKCTIEYELKYNIDSENKWTITIKNLHYKDGDLNKGIEAKINTLLPAQCTNGSEVR 119
DB 61 HPEKCTVEYELKYNIGSETWTITIKNLHYKDGDLNKGIEAKINTLLPWQCTNGSEVQ 120

QY 120 SSWAETTYWTSPOGNETKIQDMCVYNNQYLVCSWPKMGVHFDYNYQLFYWYEGLDH 179
DB 121 SSWAETTYWISPOGIEPKYQDMQDCVYNNQYLLCSWPKGIGVLDTNLYFYWYEGLDH 180

QY 180 SAECTDYIKVKNNGCRFPYLESSDYKDFYICVNGSSSQPIRPSYFIFQLQNIKVPMP 239
DB 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYTFEQLQNIKVP 240

QY 240 PLYLSITVKNSEINKNMPKGPAPKCFIYEIEFTDGTWVTTTVENETQIRTSNE 299
DB 241 PVLFTFTRESSCEIKLKSIPGLPTPARCFDIYEIREDDTFLVTATVENETFTTKTNE 300

QY 300 SOKLCFLVRKSVNIYCSDDGISEWSDQCKWG-DIWETLFFLIPAFVSIFFLVITC 358
DB 301 TQQLCFVRKSVNIYCSDDGISEWSDQCKWEGEDLSKRTLLRFLWDPFGFILLIVFVIG 360

QY 359 LLLYKORALLKTI 371
DB 361 LLLRKPNTYPKMI 373

RESULT 2
ID IL13_MOUSE STANDARD; PRT; 424 AA.
AC O09030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (Interleukin-13 binding protein) (NR4).
DE IL13RAL OR IL13RA OR IL13R.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:96133964; PubMed:8552669;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Wilson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin
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RT 13 receptor that is also a component of the interleukin 4 receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
CC -!- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
CC ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
CC ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
CC CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
CC GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY
CC SIMILARITY).
CC -!- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
CC IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, KIDNEY,
CC TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S80963; AAB50695.1; -
CC MGD; MGI:105052; IL13ral.
CC InterPro: IPR002996; CRIA.
CC InterPro: IPR003532; Hematopo_receptor_S_F2.
CC PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 25
FT CHAIN 26 424
FT DOMAIN 26 340
FT TRANSMEM 341 364
FT DOMAIN 365 424
FT DOMAIN 37 100
FT DISULFID 44 93
FT DISULFID 132 142
FT DISULFID 171 183
FT CARBOHYD 35 35
FT CARBOHYD 59 59
FT CARBOHYD 103 103
FT CARBOHYD 136 136
FT CARBOHYD 262 262
FT CARBOHYD 338 338
SQ SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F9 CRC64;

Query Match 16.2%; Score 346; DB 1; Length 424;
Best Local Similarity 27.2%; Pred. No. 1.3e-21;
Matches 110; Conservative 71; Mismatches 175; Indels 48; Gaps 17;

QY 8 VGLFYLTVCTAFGSMLSNAEIKVNPQDFEIVDYGVLGVLQWQPPLEPDNFKECTIE 67
DB 7 LGELVLLLTATVGQVA-AATEVQPPVTNLVSVENLCTIITWSP--EGASPNCTLR 63

QY 68 YELKYRNIIDSENKWTITIKNLHYKDGDLNKGIEAKINTLLPAQCTNGSEVRSSAEITY 127
DB 64 Y---FSHFDQDDKKIAPET-HRKEELPLDE---KICLVGSGCSANESEKPSPLVKC 115

QY 128 WTSPOGNETKITQDMCVYNNQYLVCSWPKMGVHFDYNYQLFYWYEGLDHSAECTDYI 187
DB 116 ISPPGDPESAFTELKCIWHNLSYMKCSWLPGRNTSPDTHYTYWYSSLEKSRQENIY 175

QY 188 KVNKNGMCRFPYLE---SSDYKDFYICVNGSSSQPIRPSYFIFQLQNIKVPMPDYL 244
DB 176 R-EGQHIAICSEKLTKEVPSFEHQNVQIMVKDAGK--IRPSCKIVSLTSYKVPDPPIKH 232

QY 245 LTVKNSEETLNKNMPKGPAPKCFIYEIEF--TEDGTTWVTTTVENETQIRTS-NE 301
DB 233 LLLKNG-ALLVQWKNPN-FRSCITYEVEVNTQTDHNLILEVEDKQCNSESQNRMBG 290

QY 302 KLCF-----LVRKSVNIYCSDDG-ISEWSDQCKWGDINKE-TLVFFLIPF 346
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Db 291 TSCFQPGVLADAVTVRVVTKNLCDFDNKLSWDSQAQ-----SIGKEQNSTFTYTM 346
Qy 347 AFVSIFVLVITCLLYKORALLKTF-----HTKKEVFSHQD 383
Db 347 LTIPFVAVAVILLFLYKRLKILIFPPIDPKGFKEMFGDQN 390

RESULT 3
IL131_HUMAN
ID IL131_HUMAN STANDARD; PRT; 427 AA.
AC P78552; O99656; O95646;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-
DE 13RA-1).
GN IL13RA1 OR IL13RA OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Carcinoma;
RX MEDLINE=97165986; PubMed=9013879;
RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,
RA Ferrara P.;
RT "Cloning of the human IL-13R alpha1 chain and reconstitution with the
RT ILAR alpha of a functional IL-4/IL-13 receptor complex.";
RL FEBS Lett. 401:163-166(1997).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,
RA Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T.,
RA Eugster H.P., Bonnefoy J.Y.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=97067184; PubMed=8910586;
RA Aman M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S.,
RA Leonard W.J.;
RT "cDNA cloning and characterization of the human interleukin 13
RT receptor alpha chain.";
RL J. Biol. Chem. 271:29265-29270(1996).
[4]
RN SEQUENCE FROM N.A.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
CC ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
CC ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
CC CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
CC GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.
CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA,
CC IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER,
CC SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND
CC KIDNEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC EMBL; Y10659; CAA71669.1; -
DR EMBL; Y09328; CAA70508.1; -
DR EMBL; U62858; AAB37127.1; -
DR EMBL; U81379; AAD00510.3; -
DR HSPF; P40189; IBQU.
DR MIM; 300119; -
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003532; Hematopo_receptor_s_F2.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT CHAIN 1 21
FT DOMAIN 22 427
FT TRANSMEM 344 367
FT DOMAIN 368 427
FT DOMAIN 39 102
FT DISULFID 134 144
FT DISULFID 173 185
FT CARBOHYD 37 37
FT CARBOHYD 61 61
FT CARBOHYD 105 105
FT CARBOHYD 138 138
FT CARBOHYD 157 157
FT CARBOHYD 235 235
FT CARBOHYD 265 265
FT CARBOHYD 293 293
FT CARBOHYD 329 329
FT CARBOHYD 341 341
FT CARBOHYD 130 130
FT CONFLICT 358 358
SQ SEQUENCE 427 AA; 48759 MW; 5983B3E8F554107B CRC64;

Query Match 14.9%; Score 318.5; DB 1; Length 427;
Best Local Similarity 25.5%; Pred. No. 2.7e-19;
Matches 105; Conservative 64; Mismatches 176; Indels 67; Gaps 19;

Qy 11 LVTLLVCTAFGMLSN-AEIKVNPQDFEIVDPGYGLYSLQWQPPFLFPDNKECTIEYE 69
Db 10 LWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNP--BGASSNCSLMY- 66
Qy 70 LAYRNIDSENWKTITKNLHYKDGFLNKGIEAKNTLL----PAQC-TNGSEVRSSNAE 124
Db 67 --FSHFGDKQDKKIAP-----ETRSIEVPLNERICLVGSCQSTNESEKPSILVE 115
Qy 125 TTYTSPQGNRETQIDMDCVYNNQYLVCSMKPGMGVHFDNTNYQLFYWYEGLDHSAECT 184
Db 116 KCI-SPPEGDPESAVTELOCIHNLSYKCSWLPGRNTSPDNTYLYWHSLEKIHQCE 174
Qy 185 DYIKVNGKMGCRFPY--LESSDYKDFYICVNGSSSQPIRPSYFIFQLQNIKVPMPDY 242
Db 175 NIFR-EGOVFGCSFDLTVKVDSFSFQHSQVQIMVKDNAGKIKPSFNIVPLTSRVKDPDPI 233
Qy 243 LSLTVKNSSEINLKNMKGPIPAKCFIYEIEFTEDGTTVTTVTVENEIQITRTSNESOK 302
Db 234 KNLSPHN-DLLXVQWENPQNTI-SRCLFYEVENVNS-----QTETHNVFYVQEAECNPE 286
Qy 303 L-----CFLV-----RSKVNLYC-SDDGIWSEWSDQCQWKGDKINKEITLV 340
Db 287 FERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCTEDDKLWSNWSQMSIGK---KRNST 343
Qy 341 FFLIPFAFVSIEVL-VITCLLYKORALLKTFHTK-----KEVFSHQD 383
Db 344 LVITMLIVPVIVAGIIVLLLYLKR-LKIIFPPIDPKGFKEMFGDQN 393

RESULT 4
IL5R_HUMAN
ID IL5R_HUMAN STANDARD; PRT; 420 AA.
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EMBL; D90205; BAA14231.1; -;
PIR; S12357; S12357.
MGI; 96558; IL5ra.
InterPro; IPR002996; CRIA.
InterPro; IPR003532; Hematopo_receptor_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 17
FT CHAIN 18 415 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.
FT DOMAIN 18 339 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 340 361 POTENTIAL.
FT DOMAIN 362 415 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 152 BY SIMILARITY.
FT FT 179 193 BY SIMILARITY.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 415 AA; 46989 MW; A4326D2922571C08 CRC64;

Query Match 12.5%; Score 266; DB 1; Length 415;
Best Local Similarity 25.7%; Pred. No. 6.5e-15;
Matches 95; Conservative 71; Mismatches 166; Indels 38; Gaps 17;

QY 8 VGFLYTLVCTAFGSMLSNAEIKVNPQDFEIVDPGYLGYLSLOWQPPFLFPD-NPEKCTI 66
DB 9 VGALATLQ-----ADLNHKKFLLPPVNTIKATG-LAQLVLLHWDPN-PDQEQRHVDL 60
QY 67 EYELKYRNIDSENWKTITKNLHYKDGFDLNGKIBAKINTLLPAOCTNGSEVRSSAEET 126
DB 61 EYHVKINAPQEDYDTRKTES---KCVTPLHGEFAASVRTILKSSHTT---LASSWVS 114
QY 127 YWTSQGRNFKIOMDCVYNN-----WQY-LVCSMKPGMGVHFDNYQLFYWVE 175
DB 115 L-KAPDGGPGTSVTLTCTTHFVSSHTLRLPYQVSLKCTWLVGKDAPEDQYFLYRFG 173
QY 176 GLDHSACTDYTK-VNGKNMGRFP--YLESSDYKDFYICVNGSSSOPRPSYFIFOLQ 232
DB 174 VL--TEKQEYSRDALNRNTACWFFRTFINSKGFQLAVHNGSSKRAIKPFDOLFSP 231
QY 233 NIVKMPDPDYLSLVKNSEELNKNMKGPIPAKCFIYEIEF--TEGTTWTTTVE 290
DB 232 ATQVNPVPRNVTEIE-SNSLYIQWEKPLSAPFDHCFNVELKIYNTKNGHIQKELIANK 290
QY 291 IQITRTSNESKLCFLVRSKVNIYCSDDGINSWSEDOCKWDIWKETLVFLIPFAFVS 350
DB 291 F-ISKIDVVS-TYSTQVRAAVSSPCRMFGWGS-QPIYVGKRRKSLVNHVLVLTAA 347
QY 351 IFVLVITCLL 360
DB 348 CFVLLIFSLI 357

RESULT 6
ID PRLR_CHICK STANDARD; PRT; 831 AA.
AC O04594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (CPRLP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.

OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE=Kidney;
RX MEDLINE=93075121; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
RL the cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL; D13154; BAA02439.1; -;
DR PIR; JQ1655; JQ1655.
DR HSSP; P14787; IAN3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 831 PROLACTIN RECEPTOR.
FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 439 459 POTENTIAL.
FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 831 AA; 94102 MW; 1C4E7579DCADBE9 CRC64;

Query Match 12.0%; Score 256; DB 1; Length 831;
Best Local Similarity 25.4%; Pred. No. 1.1e-13;
Matches 100; Conservative 58; Mismatches 161; Indels 74; Gaps 19;
QY 15 LVCTAFGSMLSNAEIKVNPQDFE---IVDPG-----YLGYSLQWQPPFLFP 58
DB 101 ITVTATNEIGNS----SDPQYVDVTSIVQPGSPVNLTLTKRSANINYLWAKWSPLLA 156
QY 59 DNFKECTTEYELKYRNIDSENWKTITKNLHYKDGFDLNGKIEAKINTL-----LPAQ 111
DB 157 DASSNHLHYELRIKPEKEWETI-----SVGVQTCQKINRLNAGMRVYVQVR 205
QY 112 CTNGSEVRSSNAEITTYWTSPQ-NRETKIQDMDCVYNNQYLVCSMKPGMGVHFDNYOL 170
DB 206 CPLDGESEWSERSHILIPSGSPPEKPTIIKRSPEKETTCWKPGLDGGHTNTYL 265
QY 171 FYWYEGLOHSAECTDYIKVNGKNMGRFPYLESSDYKDFYICVNGSSE--SQPIRPSYFI 228

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Db 266 LYSKEGEQVYECPDY--RTAGPN--SCYFDKHKHTSEFTYNIITVRATNMGSSSDPHY-- 321
QY 229 FOLQNIIVKMPDPDYLSTLVKNSEIN-----LKNWNP-----KGPFAKCFIYIEIF- 275
Db 322 VDVYIVQDPP--VNVTLKPKPKRKPKYLVLTWSPPLADVRSGWLTLE---YELRLK 376
QY 276 TEDGTTVTTTVEINEIQITRTS--NESQKLCFLVRKSVNIYCSDD--GIWSESDQCWK- 331
Db 377 PEEGEWETIEFGQQQYQKMSLPGKKYI-----IQIHCXPDHGSSESNSENYIOI 430
QY 332 -GDIWKETLVFLIPFAFVSIFVLVITCLLYK 363
Db 431 PNDFRVKDMIVMIVLGLVSLICLIMSWTWLVK 463

RESULT 7
PRLR_MELGA
ID PRLR_MELGA STANDARD; PRT; 831 AA.
AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (TPRLR).
GN PRLR.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagridae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA MEDLINE=97057891; PubMed=8902221;
RA Zhou J.F., Zagworny D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
RT prolactin receptor during various reproductive states in Meleagris
RT gallopavo.;"
RL Biol. Reprod. 55:1081-1090(1996).
[2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE=Ovary;
RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DDJB databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L76587; AAB01544.1; .
DR EMBL; U22947; AAB75038.1; .
DR EMBL; U22924; AAB75039.1; .
DR HSP; F16471; I8P3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00050; FN3; 3.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831

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FT DOMAIN 122
FT DOMAIN 123
FT DOMAIN 228
FT DOMAIN 326
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 91
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94394 MW; 220918320F77FAC1 CRC64;

Query Match 11.3%; Score 240.5; DB 1; Length 831;
Best Local Similarity 26.2%; Pred. No. 2.2e-12;
Matches 106; Conservative 53; Mismatches 154; Indels 91; Gaps 23;

QY 12 YTLIVCTAFGSMLSNAEIKVNPDPDFE---IVDPG-----YLGYSLSQWQPP 55
Db 99 YNITV--TATNEIGSNS---SDPQYVDVTSIVQPGSPVNLTLTQRYANIMYLWAKWSPP 153
QY 56 LPDFNFKECTIEVELKYRNIDSENKMTITTKNLHYKDGFDLANKGTEAKINTLLPAQCTNG 115
Db 154 LADASSNHLHYELRLKPEKEWETV-----PVGQVQCKINR--LNAGMRVY 201
QY 116 SEVR-----SSWAETTYTWS-----POGNRETKIQDMDCVYVYNWQYLVCSWKP 158
Db 202 VQVRCLMDPGWSE---WSSERRILISGGLSPPEPTITK---CRSPEKETFTCWKP 253
QY 159 GMGVHFDTNQFYWYVEGLDHAECTDYIKVNGKNMGCRFPYLESDDYKDFICVNGSSE 218
Db 254 GLDGGHPTNTLLYSKEGEQVYECPDY--RTAGPN--SCYFDKHKHTSEFTYNIITVKTATNE 311
QY 219 --SQPIRPSYFIFQIQNIIVKMPDPDYLSTLVKNSEIN-----LKNWNPCKGPIPA---- 266
Db 312 MGSNSSDPHY--VDVYIVQDPPPANVTLELK--KPINKPKYMLMTWSP--PLADVRSG 365
QY 267 -KCFIYIEIF--TEDGTTVTTTVEINEIQITRTS--NESQKLCFLVRKSVNIYCSDD--GIW 321
Db 366 WLTLDELRLKPEEGEENETVFVGGQYQKMSLPGKKYI-----YQIHCXPDHGSW 419
QY 322 SEWSEDEQWKK--GDIWKETLVFLIPFAFVSIFVLVITCLLYK 363
Db 420 SEWSSSENYIEIPNDFRVKDMIVMIVLGLVSLICLIMSWTWLVK 463

RESULT 8
CYRG_HUMAN
ID CYRG_HUMAN STANDARD; PRT; 369 AA.
AC P31785;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytokine receptor common gamma chain precursor (Gamma-C) (Interleukin-
DE 2 receptor gamma chain) (IL-2R gamma chain) (P64) (CD132 antigen).
GN IL2RG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92335883; PubMed=1631559;
RA Takeshita T., Asao H., Ohtani K., Ishii N., Kumaki S., Tanaka N.,
RA Munakata H., Nakamura M., Sugamura K.;
RT "Cloning of the gamma chain of the human IL-2 receptor.;"
RL Science 257:379-382(1992).
RN [2]

```

RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-93293887; PubMed-8514792;
 RA Noguichi M., Adelstein S., Cao X., Leonard W.J.;
 RT "Characterization of the human interleukin-2 receptor gamma chain
 RT gene.";
 RL J. Biol. Chem. 268:13601-13608(1993).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.
 RX MEDLINE-94004847; PubMed-8401490;
 RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,
 RA Willard H., Henthorn P.S.;
 RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated
 RT in X-linked severe combined immunodeficiency, SCIDX1.";
 RL Hum. Mol. Genet. 2:1099-1104(1993).
 RN [4]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE-94090315; PubMed-8266076;
 RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,
 RA Arai K.-I., Sugamura K.;
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between
 RT receptors for IL-2 and IL-4.";
 RL Science 262:1874-1877(1993).
 RN [5]
 RP IDENTIFICATION AS A IL-4R SUBUNIT.
 RX MEDLINE-94090317; PubMed-8266078;
 RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguichi M.,
 RA Leland P., Friedmann M.C., Miyajima A., Puri R.K., Paul W.E.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT Interleukin-4 receptor.";
 RL Science 262:1880-1883(1993).
 RN [6]
 RP IDENTIFICATION AS A IL-7R SUBUNIT.
 RX MEDLINE-94090316; PubMed-8266077;
 RA Noguichi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,
 RA Leonard W.J.;
 RT "Interleukin-2 receptor gamma chain: a functional component of the
 RT Interleukin-7 receptor.";
 RL Science 262:1877-1880(1993).
 RN [7]
 RP 3D-STRUCTURE MODELING OF 57-248.
 RX MEDLINE-95111955; PubMed-7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 RT modelling.";
 RL Structure 2:839-851(1994).
 RN [8]
 RP VARIANTS XSCID PHE-115; CYS-240 AND ILE-241.
 RX MEDLINE-94130970; PubMed-8299698;
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,
 RA de Saint Basile G.;
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked
 RT severe combined immunodeficiency disease result in the loss of
 RT high-affinity IL-2 receptor binding.";
 RL Eur. J. Immunol. 24:475-479(1994).
 RN [9]
 RP VARIANT XSCID LYS-68.
 RX MEDLINE-94375038; PubMed-8088810;
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Detection of three nonsense mutations and one missense mutation in
 RT the interleukin-2 receptor gamma chain gene in SCIDX1 that
 RT differently affect the mRNA processing.";
 RL Genomics 21:291-293(1994).
 RN [10]
 RP VARIANT XSCID HIS-162.
 RX MEDLINE-94300093; PubMed-8027558;
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,
 RA Konno T., Maeda M., Uchiyama T., Sugamura K.;
 RT "Impairment of ligand binding and growth signaling of mutant IL-2
 RT receptor gamma-chains in patients with X-linked severe combined
 RT immunodeficiency.";

RL J. Immunol. 153:1310-1317(1994).
 RN [11]
 RP VARIANT XSCID ASN-39.
 RX MEDLINE-95029332; PubMed-7937790;
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,
 RA de Saint Basile G.;
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X
 RT chromosome-linked severe combined immunodeficiency with peripheral T
 RT cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).
 RN [12]
 RP VARIANTS XSCID CYS-226 AND HIS-226.
 RX MEDLINE-95397841; PubMed-7668284;
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain
 RT gene causing human X-linked severe combined immunodeficiency.";
 RL Am. J. Hum. Genet. 57:564-571(1995).
 RN [13]
 RP VARIANT XSCID SER-183.
 RX MEDLINE-96013903; PubMed-7557965;
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,
 RA Levinsky R.L., Kinnon C.;
 RT "Screening for mutations causing X-linked severe combined
 RT immunodeficiency in the IL-2R gamma chain gene by single-strand
 RT conformation polymorphism analysis.";
 RL Hum. Genet. 96:427-432(1995).
 RN [14]
 RP VARIANT XSCID GLN-237 G-H-W INS.
 RX MEDLINE-95164726; PubMed-7860773;
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor
 RT gamma-chain mutation causing X-linked severe combined
 RT immunodeficiency.";
 RL J. Clin. Invest. 95:895-899(1995).
 RN [15]
 RP VARIANT XSCID GLN-293.
 RX MEDLINE-95190013; PubMed-7883965;
 RA Schmalstieg F.C., Leonard W.J., Noguichi M., Berg M., Rudloff H.E.,
 RA Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;
 RT "Missense mutation in exon 7 of the common gamma chain gene causes a
 RT moderate form of X-linked combined immunodeficiency.";
 RL J. Clin. Invest. 95:1169-1173(1995).
 RN [16]
 RP VARIANT XSCID ARG-115.
 RX MEDLINE-97042245; PubMed-8900089;
 RA Stephan V., Wahn V., Le Deist F., Dirksen U., Broeker B.,
 RA Mueller-Fleckenstein I., Horneff G., Schroten H., Fischer A.,
 RA de Saint Basile G.;
 RT "Atypical X-linked severe combined immunodeficiency due to possible
 RT spontaneous reversion of the genetic defect in T cells.";
 RL New Engl. J. Med. 335:1563-1567(1996).
 RN [17]
 RP VARIANT XSCID GLN-285.
 RX MEDLINE-97295088; PubMed-9150740;
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,
 RA Cant A., Kinnon C.;
 RT "B-cell-negative severe combined immunodeficiency associated with a
 RT common gamma chain mutation.";
 RL Hum. Genet. 99:677-680(1997).
 RN [18]
 RP VARIANT XSCID CYS-222.
 RX MEDLINE-98064061; PubMed-9399950;
 RA Sharfe N., Shahar M., Roifman C.M.;
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus
 RT morphology.";
 RL J. Clin. Invest. 100:3036-3043(1997).
 CC -!- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
 CC INTERLEUKINS.
 CC -!- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
 CC PROBABLY ALSO THE IL-13 RECEPTORS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED
 CC IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA, SWISS TYPE


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CC OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -I- DATABASE: NAME=PROW; NOTE=CD guide Cdl32 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdl32.htm".
CC -I- DATABASE: NAME=IL2Rbase; NOTE=X-linked SCID mutation database;
CC WWW="http://www.nhgri.nih.gov/DIR/GMBB/SCID/".
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CC -----
CC EMBL: D11086; BAA01857.1; -
CC EMBL: L12183; AAS59145.1; -
CC EMBL: L12178; AAS59145.1; JOINED.
CC EMBL: L12176; AAS59145.1; JOINED.
CC EMBL: L12177; AAS59145.1; JOINED.
CC EMBL: L12179; AAS59145.1; JOINED.
CC EMBL: L12180; AAS59145.1; JOINED.
CC EMBL: L12181; AAS59145.1; JOINED.
CC EMBL: L12182; AAS59145.1; JOINED.
CC EMBL: L19546; AAC37524.1; -
CC DR PIR: A42565; A42565.
CC DR PDB: 1ILM; 26-JAN-95.
CC DR PDB: 1ILN; 26-JAN-95.
CC DR MIM: 308380; -.
CC DR MIM: 300400; -.
CC DR InterPro: IPR002996; CRIA.
CC DR InterPro: IPR003961; FN.III.
CC DR InterPro: IPR003531; Hematopo_receptor_S_F1.
CC -----
Query Match 10.9%; Score 232; DB 1; Length 369;
Best Local Similarity 24.1%; Pred. No. 3.9e-12;
Matches 65; Conservative 48; Mismatches 123; Indels 34; Gaps 9;
QY 125 TTVTWTSPOGNRET-----KIQDMDCVYVNWYLVCSWKGPMGVHED 165
DB 25 TTTLT-PNGNEDTADFLLTPTDLSVSTLPLPEVQCFVNEYVNMCTNSSSPQ-P 82
QY 166 TNYQLFYWYEGLDHS--AECTDYIKYNGKMGCRFFPYLESSDYKDFYICVNGSSESOPIR 223
DB 83 TNLTLHWYKNSDNDKVKQSHVLFSEETSGCQLQKKEHLVQTFVVLQDPRE--PRR 140
QY 224 PSYFIFQLQNIKPMPPDYLSLVTKNSEINLKNWPKGPIPAKCFIYEIETFTD-GTTW 282
DB 141 QATQMLKQLNLVTPWAPENLTLLKLSQSLELNNW---NRLFNHLCLEHLVQYRTDWDHSW 197
QY 283 VTTTVEIQTIRTSNESOK-LCFLYRSKVNICYSDDGIGWSEMSDQCWKGDINWETLVF 341
DB 198 TEGSDYRIKHFLSPSDGQRRYTRFRSRPNPLCGSAQHWSEWSHPDHWGNSNTPENPEL 257
QY 342 FLIPFAFVSI-----FVLVITCLLLYKQRAL 367
DB 258 FALAEAVVISVGSMLIISLLCVYFWLERTM 287
RESULT 9
IL3B_MOUSE STANDARD; PRT; 878 AA.
AC P26954;
DT 01-OCT-1993 (Rel. 27, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-3 receptor class II beta chain precursor (Colony
DE stimulating factor 2 receptor, beta 2 chain).
GN CSF2RB2 OR A12CA OR IL3RB2 OR IL3R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90117145; PubMed=2404337;
RA Itoh N., Yonehara S., Schreurs J., Gorman D.M., Maruyama K., Ishii A.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning of an interleukin-3 receptor gene: a member of a distinct
RT receptor gene family.";
RL Science 247:324-327(1990).
CC -I- FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3
CC RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE
CC OTHER CONTAINS THE BETA CHAIN ALSO SHARED BY HIGH-AFFINITY IL-5
CC AND GM-CSF RECEPTORS.
CC -I- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M29855; AAA39295.1; -
CC DR PIR: A40091; A40091.
CC DR MGD; MGI:1339760; Csf2rb2.
CC DR InterPro: IPR002996; CRIA.
CC DR InterPro: IPR000282; Cytok_receptor_2.
CC DR InterPro: IPR003961; FN.III.
CC DR InterPro: IPR003531; Hematopo_receptor_S_F1.
CC DR Pfam: PF00041; fn3; 2.
CC DR SMART; SM00060; FN3; 2.
CC DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
CC DR Receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 22
FT CHAIN 23 878
FT INTERLEUKIN-3 RECEPTOR CLASS II BETA
FT CHAIN
FT DOMAIN 23 440
FT TRANSMEM 441 462
FT DOMAIN 463 878
FT DISULFID 39 49
FT DISULFID 78 95
FT DISULFID 254 264
FT DISULFID 293 310
FT CARBOHYD 52 62
FT CARBOHYD 350 350
SQ SEQUENCE 878 AA; 97195 MW; 8EBC9092ADC24D56 CRC64;
Query Match 10.4%; Score 221; DB 1; Length 878;
Best Local Similarity 24.5%; Pred. No. 1e-10;
Matches 86; Conservative 58; Mismatches 155; Indels 52; Gaps 19;
QY 33 PPQDFEIVDPGVLYGLSLQWQPLFPDN---PKECTIEYELKYRNTDSNWKTIITKNLH 89
DB 139 PPKDTHISPG--DHPFLLEWSVSLGDSQVSWLSKDIIEFVAYKRL-QDSWED--ASSLH 193
QY 90 YKDGFDLNGIEAKI---NTLLPA-----QCTNGSEVR---SSWAETTYTSPQGNRETKI 139
DB 194 -TSNQVN--LEPKFLPNSIVAARVTRLSAGSSLSGRPSRWSPEVHWSQPGDK-AQP 249
QY 140 QDMDCVYVNWYLVCSWKGPMGVHEDTNYQLFYWYEGLDHSAECTDYIKVNGKNM-----G 195
DB 250 QNLQCFEFDGIQSLHCSWEVMTQTGTSVSGFLFRPSAAPAEKCSPPVQPOAVTRYR 309
QY 196 CRFPYLESSDYKDFYICVNGSSESOPIRSYFIFQLQNIKPMPPDYLSLVTKNSEINL 255
DB 310 CSLPVPPEPSAHSQYTVSVKHLGQKFIIMSYHI-----QMEPPILOT-KNRDSYSL 360
QY 256 KNNMPKGPPIPAKC-FIYEIETFTDGTWTWTTTVENEIQITRTS-----NBSQKLCFLVRSK 310
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Db 361 HWETOK--IPKYIDHTFQVQYKKKSESKDKSTENLGRVNSMDLPLEPDTSYCARVRVK 418
Qy 311 -VNIYCSDDGISENSDEQCKGDIWKETLVFPLIPFAFVSIFVLVITCLL 360
Db 419 PISDY---DGIWSENSNEYTWTDWVMTLWIVLI-----LVFLIFLILL 460

RESULT 10
CYRB_MOUSE
ID CYRB_MOUSE STANDARD; PRT; 896 AA.
AC P26955;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cytokine receptor common beta chain precursor.
GN CSF2RB OR CSF2RB1 OR AIC2B OR IL3RB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319131; PubMed=1695379;
RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,
RA Yahara I., Arai K., Miyajima A.;
RT "Cloning and expression of a gene encoding an interleukin 3 receptor-
RT like protein: identification of another member of the cytokine
RT receptor gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).
CC -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5
CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC -----
DR EMBL: M34397; AAA37204.1; -.
DR PIR: A35782; A35782.
DR MGD: MGI:1339759; Csf2rb1.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR000282; Cytok_receptor_2.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003531; Hematopo_receptor_S_F1.
DR Pfam: PF00041; fn3; 2.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 896
FT DOMAIN 23 441
FT TRANSMEM 442 463
FT DOMAIN 464 896
FT DOMAIN 132 241
FT DOMAIN 343 440
FT DISULFID 39 49
FT DISULFID 77 94
FT CARBOHYD 62 62
FT CARBOHYD 141 141
FT CARBOHYD 350 350
SQ SEQUENCE 896 AA; 99111 MW; 8CE16EDFDC07A999 CRC64;

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Query Match 10.4%; Score 221; DB 1; Length 896;
 Best Local Similarity 22.6%; Pred. No. le-10;
 Matches 90; Conservative 64; Mismatches 153; Indels 92; Gaps 21;

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Qy 31 VNPQDFEIVDPGYLG-----LSLOWQPPLPDPN----- 60
Db 100 VIPYTRFSTNEDYYSFRPDSLDGIQLMPLAQNVQPP- PKNVSTSSSEDRLLEWSYS 158
Qy 61 -----FKECTIEYELKYNIDSENWKTITITKLNHYKDGFDLNGKIEAKI----- 104
Db 159 LGDAQVSWLSSKDIEFAVKRL-QDSWED--AYSILH-TSKFQVN--FEPKLFPLNSIYA 212
Qy 105 ----NTLLPAQCTNGSEVRSSWAETTYTSPQGNRETKIQDDMCVYNNQYLVCSWKPGM 160
Db 213 PRVTRFLYPCGSLSRP--SRWSPAHWDSQPGDK-AQPNLQCFPDGQLSHCSWEVWT 269
Qy 161 GYHFDITNQLFYWYEGLDHSAECTDIK-VNGKNM---GCRFPYLYESSDYKDFYICVNG 215
Db 270 QTTGVSFGLFYRPSVPAPEEKSCSPVVKPPGASVYTRYHCSLPVPEPSAHSQYTVSVKH 329
Qy 216 SSESQPIRPSYIFQLQNIIVKMPDPDYLSTVKNSEINLKNMMPKGPPIAKCFI---YE 272
Db 330 LEQCK-----FIMSYNHI--QMEPTLNLTKNRDYSLSLHWETQK---MAYSFIEHTFO 377
Qy 273 IEFTEDGTTWTTTVEINEIOITRTSNEQ---KLCFLVRSKVNIIYCSDDGIWSEWDEQC 329
Db 378 VOYKKSDSWEDSKTEN-LDRAHSMDSLQLEPDTSCARVRVKPISNYDGIWSEWDEYT 436
Qy 330 WKGD-----IWKETLVFFLIPFAFVSIFVLVITCLLLYK 363
Db 437 WKTDWVMTPLWIVLILVFLI---LTLILLRFGCVSVYR 472

RESULT 11
PRLR_COLLI
ID PRLR_COLLI STANDARD; PRT; 830 AA.
AC Q90374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosaustra; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Cropsac;
RX MEDLINE=94283267; PubMed=75168666;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin
RT receptor.";
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC -----
DR EMBL: U07694; AAA20646.1; -.
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 4.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.

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KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439
FT TRANSMEM 440 460
FT DOMAIN 461 830
FT DOMAIN 25 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 263 263
FT CARBOHYD 304 304
FT CARBOHYD 316 316
FT CARBOHYD 336 336
FT SEQUENCE 830 AA; 94507 MW; 3B074B83CDF69EFF CRC64;

Query Match 10.2%; Score 217.5; DB 1; Length 830;
Best Local Similarity 25.7%; Pred. No. 1.8e-10;
Matches 87; Conservative 53; Mismatches 158; Indels 41; Gaps 16;

QY 47 YLSLQHPPLFPDPNFECTI-EYELRYNIDSENWKTITTKNLHYKDFGLNKIEAKIN 105
Db 145 YLLAKWSPLPADVTSNSHYRYELRLKPEKEWETV---SVGVQTKVKNR-LOAGVK 200
QY 106 TLLPAQCTNGSEVRSSWAETTYTWSQG-NRETKIQDMDCVYNNMOYLYCSWKPGMGVHF 164
Db 201 YVVQVRCVLIDIGESWSESRHHIHNGESPPEKPIIKRSPKEKTFTCWKKPGSDGGH 260
QY 165 DTNYQLFYWYEGLDHSAECTDIYKVNKNMGCRFPYLESSDYKDFYICVN-----GSSSES 219
Db 261 PTNYTLLYSKEGEBRYECPDY-KTAGPN-SCYFDKKTFSFTYIYNTIKATNEIGSNVS 318
QY 220 QPIRPSYFIFQLQNIKVPMPDYLSL---TVKNSSEINLKNMKGPIPA-----KCFI 270
Db 319 DPL-----YVDYIYVQTPPVNVTLELAKTVNRKPYLVLTWSP--PLADVRSGLWLTLD 371
QY 271 YEIEF--TEDGTTWVTTVENEIQITRS-NEQKLCFLVRSKVNIYCSDD--GIWSEWD 326
Db 372 YELRLAPEAEWETIFVGQTHYKMFSLNPGKKYI-----VQIHCKPDHGHGSWSEWSL 425
QY 327 EQCWK--GDIMKETLVFFLIPFAFVSIFVLVITCLLLYK 363
Db 426 EKYLIQPTDFRIKDMVYVIIGVLSLCLVMSWTWVLK 464

RESULT 12
CYRG_CANFA
ID CYRG_CANFA STANDARD; PRT; 373 AA.
AC P40321;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cytokine receptor common gamma chain precursor (Gamma-C)
DE (interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
GN IL2RG.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=95130114; PubMed=7829104;
RA Henthorn P.S., Somberg R.L., Fimiani V.M., Puck J.M., Patterson D.F.,
RA Felsburg P.J.;
```

```
RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked
RT severe combined immunodeficiency is a homologue of the human
RL disease."
CC Genomics 23:69-74 (1994).
CC -|- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -|- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
CC SEVERE COMBINED IMMUNODEFICIENCY.
CC -|- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY III-LIKE DOMAIN.
CC -|- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U04361; AAC48403.1; -.
DR HSSP; P31785; 1ILN.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 22
FT CHAIN 23 373
FT DOMAIN 23 261
FT TRANSMEM 262 283
FT DOMAIN 284 373
FT DOMAIN 151 249
FT DISULFID 62 72
FT DISULFID 102 115
FT CARBOHYD 24 24
FT CARBOHYD 71 71
FT CARBOHYD 75 75
FT CARBOHYD 84 84
FT CARBOHYD 159 159
FT CARBOHYD 164 164
FT CARBOHYD 249 249
FT SEQUENCE 373 AA; 42516 MW; 03A0DE1F8B089D8B CRC64;

Query Match 10.1%; Score 216; DB 1; Length 373;
Best Local Similarity 25.1%; Pred. No. 8.7e-11;
Matches 70; Conservative 51; Mismatches 128; Indels 30; Gaps 11;

QY 104 INTLLPAQCTNGSE-----VRSSWAETTYTWSPOGNETRTKTQDMDCVYNNMOYLYCSW 156
Db 23 LNSTVP--MPNGNEDITPDFFLTATPSETLSVSS-----LPLPEVQCFVFNVEYNNCTW 74
QY 157 KPGMGVHFDNTNYOLFVWYBGL--DHSACTDYIKVKNMGCRFPYLESSDYKDFYICVN 214
Db 75 NSSSEPR-PTNLTTHYWKNSNDKQVOECGHYLFSEVTAGCWLQKEEIHLYETFFVYQLR 133
QY 215 GSSESQIPRPSYFIFQLQNIKVPMPDYLSTLVKNSSEINLKNMKGPIPAKCFIYEIE 274
Db 134 DPRE--PRROSTOKLKLONLVIPAPENLTNLHNSOLELSWS---NRHLDHCLHEHVQ 188
QY 275 FTED-OTTWTTVTTVENEIQITRTSNESQKL-CFLVRSKVNIYCSDDGIWSEWDEQWK 332
Db 189 YRSDWRDTSQSDVQRNSFSLPSVDGQKPYTPRVSRYNPLCGSAQRWSEWSHPHWGS 248
QY 333 DTWKETLVF---FLIPFAFVSIFVLVITCLLYKORAL 367
Db 249 NTSKENPLFASEAVLPLGSMGLIISLI-CVYWLERSI 286
```


(Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=96268473; PubMed=8672241;
RX Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
RA "Cloning and chromosomal mapping of bovine interleukin-2 receptor
FT gamma gene.";
RT DNA Cell Biol. 15:453-459(1996).
RL CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND
CC PROBABLY ALSO THE IL-13 RECEPTORS.
CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U33748; AB07812.1; -.
CC HSSP; P31785; ILN.
DR DR InterPro; IPR002996; CR1A.
DR DR InterPro; IPR003961; FN.III.
DR DR InterPro; IPR003531; Hematopo_receptor_S_Fl.
DR DR Pfam; PF000041; fn3; 1.
DR DR SMART; SM00060; FN3; 1.
DR DR PROSITE; PS01355; HEMATOPO_REC_SF1; 1.
KW KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 379 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 290 POTENTIAL.
FT DOMAIN 291 379 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 158 256 FIBRONECTIN TYPE-III.
FT DISULFID 68 78 POTENTIAL.
FT DISULFID 109 122 POTENTIAL.
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9CB032178 CRC64;
Query Match 9.3%; Score 199; DB 1; Length 379;
Best Local Similarity 24.3%; Pred. No. 2 4e-09;
Matches 68; Conservative 50; Mismatches 130; Indels 32; Gaps 11;
Qy 129 TSPGNETK---IQDMDCVYNNQYLVCWKPMGVHFDNTYQLFWY---ECLDSAE 182
Db :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
50 STPAGSTLDVSTLPKPVKQCFVFNVFNCTWNSSEPQ--PNNLTLHYGRNFNGDDKLQE 108
Qy 183 CTDYIKVGNKMCRFPYLESSDYKDFYICVNSSSE--SQPIRSFYIOLNIYKPMPP 240
Db :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
109 CGHYLFSEGITSGCFFKKKEIRLETYTEVVQLQDPREHRKQPQ----MLQDLVIPWP 164
Qy 241 DYLSLTVKNSEEENLNKNMFKPIPAKCFETYEETED-GTTWTVTTVNEIQITTSNE 299
Db :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
165 ENLTLRNLSEFQELWS---NRYLDLCHEHLVOYRSDDRSTWGSDVDRHHSFLPSVD 221
Qy 300 SKQL-CFLVRSKYNICYSDGIWNSESDCOCKGDIMKE-----TLVFFLIIPA 347
Db :||| | |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:

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Db      222  AQKLYTFVRGRYNPLCGSAQHWSDWSPYIHGWSNTSEKNTENPENPSLFALEAVLIPIG 281

Qy      348  FVSIFVLVITCLLYKORAL--LKTIFTKKEVFSHQDTF 385
      : : | : : : : : : : : : : : : : : :
Db      282  SMGLIVSLI-CVYCWLRTMPRIPLTKKNELDIVTEYQGNF 320

RESULT 15
PRLR_BOVIN
ID      PRLR_BOVIN      STANDARD;      PRT;      581 AA.
Q28172;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Prolactin receptor precursor (PRL-R).
GN      PRLR.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RS      SEQUENCE FROM N.A.
RC      TISSUE=Endometrium.
RX      MEDLINE=93246019; Pubmed=1338725;
RT      Scott P., Kessler M.A., Schuler L.A.;
RA      "Molecular cloning of the bovine prolactin receptor and distribution
RT      of prolactin and growth hormone receptor transcripts in fetal and
RT      utero-placental tissues.";
RL      Mol. Cell. Endocrinol. 89:47-58(1992).
CC      -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC      PROLACTIN.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC      -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L02549; AAA51417.1; -.
DR      HSPG; P14787; IAN3.
DR      InterPro; IPR002996; CR1A.
DR      InterPro; IPR003961; FN.III.
DR      InterPro; IPR003528; Hematopo_receptor_L_F1.
DR      Pfam; PF00041; fn3; 2.
DR      SMART; SM00060; FN3; 2.
DR      PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW      Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT      SIGNAL      1      24
FT      CHAIN      25      581
FT      DOMAIN      25      234
FT      TRANSMEM      235      258
FT      DOMAIN      259      581
FT      DOMAIN      25      122
FT      DOMAIN      123      227
FT      DISULFID      36      46
FT      DISULFID      75      86
FT      CARBOHYD      59      59
FT      CARBOHYD      132      132
SQ      SEQUENCE      581 AA; 65153 MW; 7385C0D695EE139 CRC64;

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Query Match          9.1%; Score 195; DB 1; Length 581;  
Best Local Similarity 29.6%; Pred. No. 8 Re-09;  
Matches 71; Conservative 31; Mismatches 88; Indels 50; Gaps 14;
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Oy 154 CSWKPGMGVHFDNTWYQLFYWEGLDHSACTDYIKVGKNGMCRFPYLESSDYKDFYICV 213

Db 46 CWEPGADGGLPTNTLYHKEGETLIHECPDY-KTGGPN-SCYFSKKHTSIWKMYVITV 103
Qy 214 N-----GSSESQIRPSYFIFOLQNIWKMPDPDYLSLTVKNSEE-----INLKNMP-RGP 263
| | | | : | | | | | | | | | | : | | | |
Db 104 NAINQMGISSDPL-----YVHTYVIVEPEPPANLTLELKHPEDRKPYLWIKWSPTMTD 158
| | | | : | | | | | | | | | | : | | | |
Qy 264 IPAKCFI--YEIEF-TEDGTTWVT--TTVENEIQITRTSNESQKLCFLVRSKVNIYCSDD 318
: : | | | | | | | | | | : : | | | |
Db 159 VKSGWFIIQYIEIRLKEKATDMETHFTLKOTQLKIFNL-YFGQKYLVOIRCK-----PDH 212
| | | | | | : | | | | | | | | | | : | | | |
Qy 319 GIWSEWSDEQCMK-----GDIWKETLVFFLIPFAFVSIEVL-----VITCLL 360
| | | | | | : | | | | | | | | | | : | | | |
Db 213 GIWSEWSPESSIQIPNDFPVKDTSMW-----IFVAILSAVICLIWVAVALKQYSWVTCIL 268

Search completed: September 20, 2002, 11:54:45
Job time: 144 sec

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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 13:36:07 ; Search time 108.29 Seconds
(without alignments)
3298.099 Million cell updates/sec

Title: US-09-828-995B-60
Perfect score: 1454
Sequence: 1 ggcacagagctgagtttgtg.....aaangaaaaaaaaaaaaa 1454

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_patents_NA.*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	842	57.9	1369	1	US-08-609-572-3
2	842	57.9	1369	4	US-08-841-751-3
3	842	57.9	1369	4	US-08-846-340-3
4	842	57.9	1369	4	US-08-846-344-3
5	727	50.0	1525	1	US-08-609-572-1
6	727	50.0	1525	4	US-08-841-751-1
7	727	50.0	1525	4	US-08-846-340-1
8	727	50.0	1525	4	US-08-846-344-1
9	42.2	2.9	7218	1	US-08-232-463-14
10	40	2.8	7400	1	US-08-261-663A-1
11	40	2.8	7400	5	PCT-US95-07754A-1
12	38.4	2.6	731	1	US-08-451-405A-2
13	38.4	2.6	3355	2	US-08-933-821-3
14	38.4	2.6	3355	3	US-08-960-507-3
15	38.4	2.6	3355	4	US-09-136-828-3
16	37.4	2.6	940	2	US-08-471-717-1
17	37.4	2.6	1241	1	US-07-593-657-6
18	37.4	2.6	1241	4	US-08-942-012B-3
19	37	2.5	663	4	US-08-998-416-191
20	37	2.5	854	4	US-08-998-416-534
21	37	2.5	860	4	US-08-998-416-287
22	37	2.5	1472	4	US-08-781-420-10
23	37	2.5	1472	4	US-08-781-420-12
24	37	2.5	1472	4	US-08-874-102-10
25	37	2.5	1472	4	US-08-874-102-12
26	37	2.5	1881	4	US-08-874-102-46
27	37	2.5	1881	4	US-08-874-102-48

28	36.4	2.5	789	6	5219739-8	Patent No. 5219739
29	36.2	2.5	1096	1	US-08-525-507-4	Sequence 4, Appl
30	36.2	2.5	1631	3	US-09-118-319-1	Sequence 1, Appl
31	36.2	2.5	3046	1	US-08-525-507-7	Sequence 7, Appl
32	36.2	2.5	4284	1	US-08-525-507-14	Sequence 14, Appl
33	36	2.5	3573	4	US-09-353-585-4	Sequence 4, Appl
34	35.4	2.4	2639	4	US-09-374-135-1	Sequence 1, Appl
35	35.4	2.4	3848	4	US-09-112-096-28	Sequence 28, Appl
36	35.4	2.4	5668	4	US-09-112-096-14	Sequence 14, Appl
37	35.4	2.4	51952	3	US-08-947-823-1	Sequence 1, Appl
38	35.2	2.4	4797	4	US-09-354-243B-25	Sequence 25, Appl
39	35.2	2.4	5836	4	US-09-233-086-2	Sequence 2, Appl
40	35	2.4	790	6	5194596-8	Patent No. 5194596
41	35	2.4	3138	1	US-07-867-106-4	Sequence 4, Appl
42	34.6	2.4	2081	4	US-08-235-836C-71	Sequence 71, Appl
43	34.4	2.4	1956	4	US-08-559-896B-1	Sequence 1, Appl
44	34.4	2.4	3126	2	US-08-477-396A-3	Sequence 3, Appl
45	34.2	2.4	518	1	US-08-485-284A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-609-572-3
; Sequence 3, Application US/08609572
; Patent No. 5710023
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,572
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103...1245
US-08-609-572-3

Query Match		57.9%;	Score 842;	DB 1;	Length 1369;
Best Local Similarity		80.6%;	Pred. No. 1.3e-206;		
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Db	69	GAGGGAATATCAAGGTTTAAATCTCGGAGAAATGGCTTTCGTTTGGCTATCGG	128		
QY	210	attcctctataccctgctgttgcacagcatttgct---ctatgcttccaatgcta	266		
Db	129	ATGCTTATATATACCTTCTCATTAAGCACACATTTGGCTGTACTTCTATCTTCAGACACCGA	188		
QY	267	gataaaagttaactcctcctcaggattttgagatagtggaacctggatatttggttatct	326		
Db	189	GATAAAAGTTAAACCTCCCTCAGGATTTTTCAGATAGTGGATCCGGATACTTAGGTTATCT	248		
QY	327	ctctttgcaatggcaacctccatttattccgggataattttaagggaatgcacaaatgaata	386		
Db	249	CTATTGGCAATGGCAACCCCACTGCTCTGGATCATTTTAAAGGAATGCACAGTGGAAAT	308		
QY	387	tgaattaaaaataccgaacattgatgtgaaactggaagaccatcattaccaagaatct	446		
Db	309	TGAACATAAATACCGAAACATTTGGTAGTGAACATGGAAGACCATCATTTACTAAGAACT	368		
QY	447	acattacaagaatgggttgatctttaacaaggtattgaagcaagataaaacacactct	506		
Db	369	ACATTTACAAAGATGGGTTTGATCTTAAACAAGGCAATGAAGCGAAGATACACACGCTTT	428		
QY	507	gcagcaccaatgcacaaatggatcgaagcttagaagttcatcctgggcagaacactactattg	566		
Db	429	ACATGGCAATGCACAAATGGATGAGAAGTTCAAAGTTCCTGGCAGAAACTACTTTATTG	488		
QY	567	gacatcaccacaagaaacgaggaaactaaaattccaagatatggactgtgtattacaaa	626		
Db	489	GATATCACCAACAGAAATTCAGAAACTAAAGTTCAGGATATGGATTGGTATATTACAA	548		
QY	627	ctggcaaatattagctgtctgtcctggaaacctggcattgggtgtccatttttgataccaa	686		
Db	549	TTGGCAATATTTACTCTGTCTTGGAAACCTGGCATAGGTGACTTCTTGGATACCAATTA	608		
QY	687	ccagtggtttactggtatgaggtcttgaccattcagcagagtgactgattacataaa	746		
Db	609	CAACTTGTTTACTGTATGAGGGCTTGGATCATGCATTTACAGTGTGTGATTACATCAA	668		
QY	747	ggtaattggaataaaatggtgagtcagggtttccctcatttggagtcacagactataaaga	806		
Db	669	GGCTATGCACAAAATATAGGATGCAGATTTCCCTATTTTGGAGGCATCAGATATAAAGA	728		
QY	807	ttctacactcgtgttaattcgggtcatcagaaatcccgccctatacagaccagctatttat	866		
Db	729	TTTCTATATTTGTTGTTAATGGATCATCAGAGAACAAAGCCTATCAGATCCAGTTATTAC	788		
QY	867	tttccagctcgaataatagtttaaacctatgcacagactacccttagcttactgtgaa	926		
Db	789	TTTTCAGCTTCAAAATATAGTTAAACCTTTGGCGCAGTCTATCTTTACTTTTACTCGGA	848		
QY	927	gaattcagaggaataataacctgaaatcggaactgacctaaagaccattccagccaatcg	986		
Db	849	GAGTTTCATGTGAATTAAGCTGAATGGAGCATACCTTTGGGACCTATTTCCAGCAAGGTG	908		
QY	987	ttctatttatgaattgaattcaacagagatggttactacttgggtgactaccacagttga	1046		
Db	909	TTTTGATTATGAATTTGAGATCAGAGAGATGATACCTTTGGTGTGCTACAGTTTGA	968		
QY	1047	gaatgagatacaaaacacaaacatcaaatgaagccaaataattatgcttttttggtgaag	1106		
Db	969	AAATGAACATACACTTGGAAACCAACAAATGAACCCGACAAATATGCTTTGTAGTAAG	1028		
QY	1107	aagttaagtgaattatttctcagatgtagtggaatcctggagtgagtgatgaacaa	1166		
Db	1029	AAGCAAGTGAAATATTATTGCTCAGATCGCGAATTTTGGAGTGTGAGTGATAAACA	1088		
QY	1167	atcgtggaaggtgta---catatggaaggaacaccttagtatttttcttgataccattgc	1223		

Db	1089	ATGCTGGGAGGFGAAGACCTATCGAAGAAACTTTGCTACGTTTCTGGCTACCATTTGG	1148
QY	1224	ttttgctcctaattttggttggtaataacttgcctgtcttttgataagaagggctttt	1283
Db	1149	TTTCACTCTTAATATTAGTTATTTGTAACCGGCTCTGCTTTTGGTAAGCAACACCTA	1208
QY	1284	actgaaacgat-----ctttcacaaaaaagaagctcttttctcatcaagacacat	1336
Db	1209	CCAAAAATGATCCAGAAATTTTCTGTATACATGAAGACTTTCCATATCAAGAGACAT	1268
QY	1337	tctgttgactcagtaactttcagctcttattggccagatgtttaaatatgagctcttataaac	1396
Db	1269	GGTATTGACTCAACAGCTTTCCAGTC--ATGGCCAATGTTCAATATGAGTCTCAATAAAC	1326
QY	1397	tgaagcttttctcctaataattgaataaa	1424
Db	1327	TGAATTTTCTTTCGCGAAAAAATAAAAA	1354

RESULT 2
US-08-841-751-3
; Sequence 3, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Donaldson, Mary
; APPLICANT: Filtz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
US-08-841-751-3


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Query Match          57.9%; Score 842; DB 4; Length 1369;
Best Local Similarity 80.6%; Pred. No. 1.3e-206;
Matches 1038; Conservative 0; Mismatches 235; Indels 15; Gaps 4;

QY 150 gagtggaactccaagtattgaactcttgaggagaatgctttccattcaatcatttgagtgcgg 209
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DB 69 GAGAGGCAATATCAAGGTTTAAATCTCGGAATAATGGCTTTCGTTGCTTGCTGCTATCGG 128
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QY 210 attctctataccctgctgttggcacagcatttgct---ctatgcttccaaatgctga 266
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DB 129 ATGCTTATATACCTTCTGATAAGCACACATTTGGCTGTACTTTCATCTTCAGACACCGA 188
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QY 267 gataaagttaactcctcctcaggatttgagatagtgaccctcgatatattgagttatct 326
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DB 189 GATAAAGTTAACCTCCTCAGGATTTTGAGATAGTGGATCCCGGATACCTTAGGTTATCT 248
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QY 327 ctctttgcaatggcaacctccattatttccggatataatttttaaggaaatgcacaaatagaata 386
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DB 249 CTATTTGCAATGGCAACCCCACTGCTCTGTGATCATTTTAAAGGAATGCACAGTGGAAAT 308
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QY 387 tgaattaaaaaccgaaacattgtagtgaaaactgggaagaccatcattaccaaagaatct 446
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DB 309 TGAACATAAAATACCAAAACATTTGGTAGTGAACATGGAAGACCATCATTTACTAAGNATCT 368
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QY 447 acattcacaagaatgggtttgatcttaacaaaggtattgaagcaaaagataaaacacacttct 506
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DB 369 ACATTACAAGATGGTTGATCTTAAACAAGGGCATTTGAAGCGAAGATACACACGCTTTT 428
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QY 507 gccagcacaaatgcacaaatggatcagaagttagaagttcattgggcagagaactactatttg 566
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QY 567 gacatcacacaaagaaatcgggaactaaaatcaaagattgactgtgtatatatacaa 626
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DB 489 GATATCACCAAGAAATTCAGAAACTAAAGTTTCAAGATATGGATGGCTGTATATTACAA 548
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QY 627 ctggcaatatatttagtctctctggaacctggcctggcctggcctattttgtataccaatta 686
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QY 687 ccagttgtttactggtatgagggcttggaccattcagcagagagtgactgattacaataca 746
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DB 609 CAACCTGTTTACTGGTATGAGGGTGGATCATGCATTTACAGTGTGTTGATTACATCAA 668
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RESULT 3
US-08-846-340-3
; Sequence 3, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103..1245
; US-08-846-340-3
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Query Match 57.9%; Score 842; DB 4; Length 1369;
Best Local Similarity 80.6%; Pred. No. 1.3e-206;
Matches 1038; Conservative 0; Mismatches 235; Indels 15; Gaps 4;

QY 150 gagggaactcaagattgaattggaaggaatggctttcattcattcattgagtgctgg 209
DB 69 GAGAGCAATATCAAGGTTTAAATCTCGGAGAAATGGCTTTCGTTTGGCTATCGG 128
QY 210 attcctctaacctgctgtttgacagcatttgctcttctgctcttcaaatgctga 266
DB 129 ATGCTTATATATCTTCTGATTAAGCACACATTTGGCTGTACTTCTATCAGACCGA 188
QY 267 gataaaagttaattcctcctcagattttgagatagtgagaccctggatatttggttatct 326
DB 189 GATAAAAGTTAAACCTCCCTCAGGATTTTTCAGATAGTGGATCCGGATACTTAGTTATCT 248
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DB 489 GATATCACCAAGGAATTTCCAGAAACTAAAGTTTCAGGATATGGATTGCGTATATACAA 548
QY 627 ctggcaatatattagttctgtctctggaacacctggcattgggttccattttgataccaatta 686
DB 549 TTGGCAATATTTACTCTGTCTTCTGGAACCTGGCATAGGTACTTCTTGATACCAATTA 608
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DB 789 TTTTCAGCTTCAAAATATAGTTAAACCTTTGGCGGAGTCTATCTTACTTTTACTCGGA 848
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DB 849 GAGTTCACTGAAATTAAGCTGAATGGAGCATACCTTTGGGACCTATTTCCAGCAAGGTG 908
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DB 909 TTTTGTATTAATTAAGATGAGATGAGAGATGATACCTTTGGTGACTGCTACAGTTGA 968
QY 1047 gaatgagatacaaatcacagaacatcaaatgaagccaaataattgctttttggtaag 1106
DB 969 AAATGAACATACCTTTGAAACCAACAAATGAAACCCGACCAATATGCTTTGTAGTAAG 1028
QY 1107 aagtaagtgaaattatttctcagatgtaggaatcctgagtgagtgagtgatgaaca 1166
DB 1029 AAGCAAGTGAAATATTTATTTGCTCAGATCAGCAATTTTGGAGTGAGTGAGTAAACA 1088
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DB 1089 ATGCTGGGAGGTGAAGAGCTATCGAAGAAACTTTTGTACGTTTCTGGCTACCATTTGG 1148
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DB 1149 TTTTCATCTTTAAATATAGTTATATTTGTAACCGGTCTGCTTTTGGCTAAGCCAAACCTA 1208
QY 1284 actgaaacagat-----ctttcatcaaaaaaagaagtccttttctcatcaagacacat 1336
DB 1209 CCAAAAATGATTCAGAAATTTTCTGTGATACATGAAGACTTTCATATCAAGAGACAT 1268
QY 1337 tetgtgactcagtaacttccagttcttattgcccagatgtttaaataatgagtccttattaaac 1396
DB 1269 GGTATTGACTCAACAGTTCCTCAGTC--ATGGCCAAATGTTCAATATGAGTCTCAATAAAC 1326
QY 1397 tgaagcttttctcccaaaattgaataaa 1424
DB 1327 TGAATTTTCTTTCGGAATAAAAAA 1354

RESULT 4
US-08-846-344-3
; Sequence 3, Application US/08846344
; Patent No. 6268480
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitzer, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,344
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1369 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 103...1245
US-08-846-344-3

Query Match 57.9%; Score 842; DB 4; Length 1369;
Best Local Similarity 80.6%; Pred. No. 1.3e-206;
Matches 1038; Conservative 0; Mismatches 235; Indels 1

4:

QY	150	gagtgaaactctcaagatgtaatactctggaggaaatggctcttcattccatttgatgtcg	209
DB	69	GAGAGCAATATCAAGGTTTAAATCTCGGAAATGGCTTTCGTTTGGCTATPCGG	128
QY	210	attcctataccctgctgttgccacagcattggct--ctatgctttccaatgctga	266
DB	129	ATGCTTATATACCTTCTTGATAAGCACAAATTTGGCTGTACTTCATCTTCAGACACCGA	188
QY	267	gataaagttaactcctcctcaggatttggatagtgagcactggatatttaggttatct	326
DB	189	GATAAAGTTAAACCTCCTCAGGATTTTGAGATAGTGATCCCGGATCTTAGGTTATCT	248
QY	327	cctcttgaatggaaacctccaattattccggataaattttaaggaaatgcacaatagata	386
DB	249	CYATTTGCAATGGCAACCCCCACTCTCTCTGGATCATTTTAAAGAAATGCACAGTGAATA	308
QY	387	tgaattaaaataccgaaacattgagtgaaactggagaccatcataccagaactct	446
DB	309	TGNACTAAAATACCGAAACATTTGGTAGTGAACATGGAAGACCATCTACTAAGAACTCT	368
QY	447	acattacaagatgggtttgatacttaacaaaggatttgaagcaagaataaacactctct	506
DB	369	ACATTTACAAGATGGGTTTGATCTTTAAGCAGGGATTTGAAGCAAGATACACACGCTTTT	428
QY	507	gccagcacaaatgcacaaatggatcagaagtttagaagttcattgagcagaacactctattg	566
DB	429	ACCATGGCAATGCACAAATGGATCAGAGTTCAAAGTTCTTGGCAGAAACTACTTATTG	488
QY	567	gacatcaccacaaggaatcgggaaactaaaattcaagatatgagctgtgtatatcaaa	626
DB	489	GATATCACACAAAGGAATTCAGAAACTTAAAGTTTCAGGATATGGATTCGGCTATATTACAA	548
QY	627	ctggcaatatttagtctctcttgaaacctggcatgggtctccattttgaacccaatta	686
DB	549	TTGGCAATATTTACTCTGTCTTTGGAAACCTGGCATAGGTGTACTCTTGATACCAATTA	608
QY	687	ccagttgttttactggtatgagggcttggacattccagcagagtgtactgattacatcaa	746
DB	609	CAACTTTGTTTACTGATGAGGGCTTGATCATGCATTACAGTGTGTGATTACATCAA	668
QY	747	ggttaatgaaaaataatggatgcaggtttccctatttggagtcatacagactaaaga	806
DB	669	GGCTGATGACAAAATATAGSATGCAGATTTCCCTATTTGGAGGCATCAGACTATAAGA	728
QY	807	ttctacatctgttgaatgggtcatcagaatccccagcctatcagaccagctatttat	866
DB	729	TTTCTATATTTGTGTTAATGGATCATCAGAGNACAAGGCTATCAGATCCAGTTATTTTAC	788
QY	867	tttcagcttcaaaaatagtttaaacctatgccaccagactaccttagtcttactgtgaa	926
DB	789	TTTTTCAGCTTCAAAATATAGTTTAAACCTTTGCGGCAGTCTATCTTACTTTTACTCGGA	848
QY	927	gaattcagaggaaataaactgaatggaacatgccataaaggacccattccagacaaatg	986
DB	849	GAGTTTCTGTGAAATTAAGCTGAATGGAGCATACCTTTGGAGACTATTTCCAGCAGGTG	908
QY	987	tttcatattatgaattgaattcacagagatgggtactacttgggtgactaccacagttga	1046
DB	909	TTTTTGATTTATGAATTTGAGATCAGAGAAAGATGATACTACCTTGGTGTACTGTACAGTTGA	968
QY	1047	gaatggatatacaaatcacaagaacatcaaatgaaaggccaaaattatgcttttggtaag	1106
DB	969	AAATGAAACATACACCTTGAAACCAACAAATGAAACCCGACAATATGCTTTGTAGTAAG	1028
QY	1107	aagttaagtgaatatatttctcagatgaggaactctggagctgagtgagtgatgaaca	1166
DB	1029	NACAAAGTGAATATTTTGTCTAGATGACGGAATTTGGAGTGGTGGAGTGATAAACA	1088
QY	1167	atgctggaaaggtga---catatggaaaggaaaccttagtatattttcttctgaaccatttgc	1223

Query Match 50.0%; Score 727; DB 1; Length 1525;
Best Local Similarity 72.5%; Pred. No. 3.7e-17;
Matches 1033; Conservative 0; Mismatches 361; Indels 3

BEST LOCAL SIMILARITY: 72.3%, FREQ NO: 3.76 177,
Matches 1033: Conservative 0; Mismatches 361; Indels 30; Gaps 6;

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QY 97 aggaactgtgataaattggcctatgataattcattctcttgagaacccattatttgatgga 156
Db 169 AGGTCTTGTGATAAATCGCTGTGATAATACATTTCTTGAGAAACCATATATTGAGTAGA 228
QY 157 aacttcaaaagtattgaattcttgaggagaatggctttcattcatttgatcgagattccctc 216
Db 229 GCTTTACAGACACTAAATCCTGGAGAAATGGCTTT-----TGTGCATATCAGATGCTTG 282
QY 217 tataccctctgtttgcacagcatttggctctctatgcttccaaatgctgagataaaagt 276
Db 283 TGTTCATCTCTCTTGTGTAACAATAACTAGCTAT-----TCCTGGAGATAAAGTT 333
QY 277 aatccctccagattttgagatagtgagccctggatattttaggttctctctctttgcaa 336
Db 334 AATCCTCCCTCAGGATTTTGAATAATTGGATCCTGGATTACTTGGTTATCTCTATTTCGAA 393
QY 337 tggcaacctccatttccggataattttaaggaatgcacaaatagaataatgaattaaaa 396
Db 394 TGAACACCTCCTGTGGTTTATAGAAAATTTAAGGGCTGTACACTAGAAATATGAGTTAAAA 453
QY 397 taccgaacattgtagtgaactggagaaccattaccacaaagaatctacattacaaa 456
Db 454 TACCGAATTTGATAGCCACAGCTGGAAGACTATAATTTACTAGGAATCTAATTTACAG 513
QY 457 gatgggttgattttaacaaaggatttgaaagcaagataaaacacactctgcagacaaa 516
Db 514 GATGGGTTTTGATCTTAATAAGGCCATTGAAGGAAGATACGTACGCATTTGTACAGCAT 573
QY 517 tgcacaaatggatcgaaacttgaagtctcatgggcagaacacttattggacatcacca 576
Db 574 TGTACAAATGGATCAGAACTCAAGTCCATGGATAGAAGCTCTTTATGGGATATCAGAT 633
QY 577 caaggaaatcgggaaactaaaatccaagatatggactgtgtattacacactggcaaat 636
Db 634 GAAGGAAGTTTGGAACTAAATTCAGGACATGAAGTGTATATATTATACTGGCAGTAT 693
QY 637 ttagtgcctctgaaacctggcattgggtgtccatttttgatcaccaattaccagttgttt 696
Db 694 TTGGTCTGTCTTGGAACTGGCAGACAGTATATTTCTGATACCAACTATACCATGT 753
QY 697 tactggtatgagggcttgaccattcagcagagtgactgattacatacgaagttaatgga 756
Db 754 TTCTGTATGAGGGCTTGGATCATGCTTTACAGTGTGCTGATTTACCTCCAGCATGATGAA 813
QY 757 aaaaatattgggtgcagggtttccctatttggagtcacagactataaagattttctacatc 816
Db 814 AAAAAATGTTGGATGCAAACTGCAAACTTGGACTCATCATCAGACTATAAAGATTTTATC 873
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Db 874 TGTGTTAATGGATCTTCAAAAGTTGGAACCCATCAGATCCAGCTATACAGTTTTTCACT 933
QY 877 caaaatattgattaaacctatgccacagactaccttagtcttactgtgaagaattcagag 936
Db 934 CAAAATATAGTTAAACCATTTGCCACCAGAAATTCCTTCATATTAGTGTGGAGAAATCCATT 993
QY 937 gaaattaaacctgaaattggaacatgcctaaaggaccattccagccaaatgttttcattat 996
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QY 1117 aatatttattgctcagatgatgaatctgagtgagtgagtgatgaacaatgctgaaa 1176
Db 1174 ATATATATATTGTCAGATGATGAATTTGAGCGAATTTGAGAGGAATTTGGGAA 1233
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Db 1234 GGTTCACACAGGGCCAGACTCAAAAGATTATTTTCATAGTACCAGTTGCTTTTCTTATA 1293
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Db 1414 AATTTCTTGACATAGAGCAG----CCAGCAGAGTCAATATTAACTCAA-TTTCCTTTA 1468
QY 1411 aaatattgataaattcttatttttaaaangaaaaaataaaaaa 1454
Db 1469 AAATTTGGAATACATCTTCTTGAAATCCAAAAAATAAAAAA 1512

RESULT 6

US-08-841-751-1
; Sequence 1, Application US/08841751
; Patent No. 6214559
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; Zip: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,751
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWN, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:

NAME/KEY: CDS
LOCATION: 256...1404
us-08-841-751-1

Query Match 50.0%; Score 727; DB 4; Length 1525;
Best Local Similarity 72.5%; Pred. No. 3.7e-177; Indels 30; Gaps 6;
Matches 1033; Conservative 0; Mismatches 361;

Qy 37 aggaaggaagctcttagagattctaataatgctcccaactggagaagagaaaaaag 96
Db 113 AGGAGGAAACACGTAGAGATTCAATTTAGTCTCT- ---AATGCGAAAGGAGACAAAG 168
Qy 97 aggaacctgataaattgacctatgataatcatcttctbtagaaaccatattattagtgga 156
Db 169 AGGTCTTGATTAACCTGCTGTGATAATACATTTCTTGAGAAACCATATTATTGAGTAGA 228
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Db 229 GCTTTTCAGCACACTAAATCCCTGGGAAATGGCTTT- ----TGTCATATACAGTGCCTTG 282
Qy 217 tataacctgctgtttgacagcatttgctctctatgctttcaaatgctgagataaaagt 276
Db 283 TGTTTCATCTCTTTGTACATAACTGGCTAT- -----TCCTTGAGATAAAAGTT 333
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Qy 337 tggcaacctccattattcccgagataatttttaagggaatgcacaaatagaataaa 396
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Qy 757 aaaaatatgggatgcaggtttccctattttggagtcacagactataaagatttctacatc 816
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Qy 877 caaaatatagtttaacctatgcccacagactacccttagtcttactgtgaagaattcagag 936
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Qy 937 gaaattaacctgaatggaactgctaaaggaccattccagccaaatgtttctatttat 996
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Qy 997 gaattgaattcacagagagtggtactactcttggtgactaccacagttgagatagata 1056
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Db 1469 AAATTCGAATACATCTTCTTGTAAAATCCAAAAAATAAAAAA 1512

RESULT 7
US-08-846-340-1
; Sequence 1, Application US/08846340
; Patent No. 6248714
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Donaldson, Debra
; APPLICANT: Fitz, Lori
; APPLICANT: Neben, Tamlyn
; APPLICANT: Whitters, Matthew
; APPLICANT: Wood, Clive
; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,340
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,572
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 256...1404
US-08-846-340-1

Query Match 50.0%; Score 727; DB 4; Length 1525;

Best Local Similarity 72.5%; Pred. No. 3.7e-177;

Matches 1033; Conservative 0; Mismatches 361; Indels 30; Gaps 6;

QY 37 aggaaggggaagcttagagattcttaatttaattgctccaaactggagaagagaaaaaag 96
DB 113 AGGAAGGAAACAGTAGAGATTCAATTTAGTGTCT----AATGTGGAAGGAGGACAAAG 168
QY 97 aggaactgtgataaattgacctatgaataattcattctcttgagaaccatattattgagtga 156
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DB 229 GCTTTTCAGCACACTAAATCTCGAGAAATGGCTTT-----TGTGCATATCAGATGCTTG 282
QY 217 tataacctgctgttggosacgacattggctctctatgcttccaatgctgagataaaagt 276
DB 283 TGTTCATTCTCTTTGTACAATAAGTGGCTAT-----TCTTTGGAGATAAAAGTT 333
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QY 697 tactggtatagggtctggaccattcagcagagtgtagtattacatacaagggttaagtga 756
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QY 817 tgtgttaattggtcatcagaatcccgctcatcagaccagctatttttttttcagctt 876
DB 874 TGTGTTAATGGATCTTCAAAAGTTGGAACCCCATCAGATCCAGCTATACAGTTTTTTCAACTT 933

QY 877 caaaatatagtttaaaccttatgcaccagactaaccttagtcttactagtgaagaattcagag 936
DB 934 CAAAATATAGTTAAACCATTTGCCACAGAAATTCCTTCATATTAGTGTGGAGAAATTCATT 993
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QY 997 gaaattgaattcacagaggttagtactacttgggtgactaccacagattgagaaatgagata 1056
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RESULT 8

US-08-846-344-1

; Sequence 1, Application US/08846344

; Patent No. 6268480

; GENERAL INFORMATION:

; APPLICANT: Collins, Mary

; APPLICANT: Donaldson, Debra

; APPLICANT: Fitz, Lori

; APPLICANT: Neben, Tamlyn

; APPLICANT: Whitters, Matthew

; APPLICANT: Wood, Clive

; TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,344

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/609,572

; FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1404
US-08-846-344-1

Query Match          50.0%; Score 727; DB 4; Length 1525;
Best Local Similarity 72.5%; Pred. No. 3.7e-177;
Matches 1033; Conservative 0; Mismatches 361; Indels 30; Gaps 6;

Qy 37 aggaagggaagctcttagagattctaataatgtctccaaactggagagagaaaaaaag 96
Db 113 AGGAAGGAAAAACAGTAGAGATTCAATTTAGTGTCT----AATGTGAAAGGAGGACAAAAG 168

Qy 97 aggaacctgataattgctctgataaattcatttcttctgagaaaccattatttagtgga 156
Db 169 AGGCTCTTGATGAACCTGCTGTGATAAATACATATTTCTTGAGAAACCATTATTTAGTAGA 228

Qy 157 aactcaaaagtatgaactctggaggaatgctttcattcatttggatgctggaattcctc 216
Db 229 GCTTTCACACACATAATCTCGGAGAAATGGCTTT-----TGTCATATCAGATGCTGTG 282

Qy 217 tataacctgtgtgttcacagcatttggctctctatgctttcaaatgctgagataaaagt 276
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Qy 277 aatcctctcaggatttggagatgaggaacctggatatttaggtatctctcttggcaa 336
Db 334 AATCCTCTCAGGATTTTGAATAATTTGGATCTGGATTACTTGGTTATCTCTATTATTGCAA 393

Qy 337 tggcaacctccattatttcccgataattttaagaatacacaaatagataatgaattaaaa 396
Db 394 TGGAAACCTCTGTGTTATAGAAAAATTTAAGGCGCTACACTAGATAATGAGTTAAAA 453

Qy 397 taccgaaacattgtagtgaaaactggagaccattaccagaagaatctacattacaaa 456
Db 454 TACCGAAATGTTGATAGCGACAGCTGGAAGACTATAATTAAGTAATCTAATTTACAAAG 513

Qy 457 gatgggttgatcttaacaaaggattttaagaacaaagataaaacacctctgcccagacaa 516
Db 514 GATGGGTTTGATCTTAATTAAGGATTTAAAGGCAATTAAGGAAATACGTACGCAATTTGTCAGAGCAT 573

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Db 574 TGTACAAATGGATCAGAAGTACAAGTCCATGGATAGAGGCTCTTATGGGATATFCAGAT 633

Qy 577 caaggaatacgggaaactaaataaagatatggaactgtgtatattacaactggcgaat 636
Db 634 GAAGGAAGTTTGGAACTAAATTAACGACATGAAGTGTATATATTAACATGGCAGAT 693

Qy 637 ttactgtctcttggaaacctggcatgggtgtccatttggataccaataacagttgttt 696
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Qy 697 tactgtatagggtctggaccattcagcagagtgatgattacatcaaggttaattgga 756
Db 754 TTCTGGTATGAGGCTTGATCATGCCCTACAGTGTGCTGATTACCTCCAGCATGATGAA 813
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Qy 757 aaaaatgggatgcaggtttccctatttggagtcacagacataaaagatttctacatc 816
Db 814 AAAAAATGTTGGATGCAAACTGTCCAACCTGGACTCATCAGACTATAAAGATTTTTTATC 873

Qy 817 tgtgtaaatgggtcctcagaaatcccagcctatcagaaccagctatttattttcagctt 876
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Qy 877 caaaatagtttaaaccttatgccaccagactaccttagcttactgtggaagattcagag 936
Db 934 CAAAATATAGTTAAACCATTTGCCACCAGAAATTCCTTCATATTAGTGTGAGAAATTCAT 993

Qy 937 gaaataaacctgaaatggaaacatgcctaaagaccacctccagccaaaatgtttcattat 996
Db 994 GATATTAGAAATGAAATGGAGCACACCTGGAGGACCCATTCACCAAGGTGTGTACACTTAT 1053

Qy 997 gaaattgaattcacagaggatggtactacttgggtgactaccacagtgagaaatgagata 1056
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Qy 1351 aacttctagttcttggccagatgttaaataatgactcttataaaactgaagcttctc 1410
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Qy 1411 aaattgaaataaattctatttttaaaangaaaaaiaaaaaa 1454
Db 1469 AAATTTCCAAATACATCTTCTTGAANAATCCAAAAAIAAAAAAAAAA 1512
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RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
;
US-08-232-463-14

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Best Local Similarity 2.7%; Pred. No. 0.17;
Matches 8; Conservative 171; Mismatches 114; Indels 0; Gaps 0;

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QY 963 taaaggaccattccagccaaatgttctattatgaattgaattcacagagatggtac 1022
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QY 1083 ccaaaaaattatcttttggtaagaagtaagtgaatatttttctcagatgatggaat 1142
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RESULT 10
US-08-261-663A-1
; Sequence 1, Application US/08261663A
; Patent No. 5571706
; GENERAL INFORMATION:
; APPLICANT: Baker, Barbara J
; APPLICANT: Whitam, Steven A
; TITLE OF INVENTION: Plant Virus Resistance Gene and Methods
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Margaret A. Connor, USDA-ARS
; STREET: 800 Buchanan Street
; CITY: Albany
; STATE: CA
; COUNTRY: USA
; ZIP: 94710
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/261,663A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Connor, Margaret A
; REGISTRATION NUMBER: 30043
; REFERENCE/DOCKET NUMBER: 0094.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 559-6067
; TELEFAX: (510) 559-5777
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana glutinosa
; TISSUE TYPE: leaf
; FEATURE:
; NAME/KEY: exon
; LOCATION: Join(294..772, 1003..2098, 2941..3213, 5032..6600,
; LOCATION: 6934..6951)
; FEATURE:
; NAME/KEY: intron
; LOCATION: 773..1002
; FEATURE:
; NAME/KEY: intron
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; FEATURE:
; NAME/KEY: intron
; LOCATION: 6601..6933
; FEATURE:
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US-08-261-663A-1

Query Match 2.8%; Score 40; DB 1; Length 7400;
Best Local Similarity 43.9%; Pred. No. 0.64;
Matches 172; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

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QY 969 accattccagccaaatgttctattatgaattgaattcacagagatggtactacttg 1028
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QY 1089 attatgcttttggtaagaagtaaaatatttttctcagatgataggaaatctggag 1148
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QY 1149 tgagtgagtgatgaacaatgctggaagtgacatatggaaggaacaccttagtttt 1208
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Db 2635 TAACATCAGTATTTCTTAAAGAAATCCAAATTTGATGTTTAACTTTGGTATTGT 2694

QY 1209 cttgataccatttggctctcaattttgttggtaataaactgacctgttttga 1268
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QY 1269 taagcaaaaggcttctactgaaacgatcttc 1300
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 17:13:36 ; Search time 559.18 Seconds
(without alignments)
4464.383 Million cell updates/sec

Title: US-09-828-995B-60
Perfect score: 1454
Sequence: 1 ggcacgagctgagttgtg.....aaangaaaaaaaaaaaaa 1454

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	%		Length DB	ID	Description
		Match				
1	1453	99.9	1454	22	AAS59962	Canine interleukin
c 2	1453	99.9	1454	22	AAS59963	Canine interleukin
3	1158	79.6	1158	22	AAS59964	Canine interleukin
c 4	1158	79.6	1158	22	AAS59965	Canine interleukin
5	1095	75.3	1095	22	AAS59966	Canine interleukin
c 6	1095	75.3	1095	22	AAS59967	Canine interleukin
7	947.8	65.2	954	22	AAS59968	Canine IL-13R extr
c 8	947.8	65.2	954	22	AAS59969	Canine IL-13R extr
9	947.8	65.2	1686	22	AAS59970	Canine IL-13R/IgG-

c	10	947.8	65.2	1686	22	AAS59971 Canine IL-13Ralpha
c	11	947.8	65.2	1686	22	AAS59976 Canine IL-13R/IgG-
c	12	947.8	65.2	1686	22	AAS59977 Canine IL-13Ralpha
c	13	947.8	65.2	1692	22	AAS59974 Canine IL-13R/IgG-
c	14	947.8	65.2	1692	22	AAS59975 Canine IL-13Ralpha
c	15	947.8	65.2	1698	22	AAS59972 Canine IL-13R/IgG-
c	16	947.8	65.2	1698	22	AAS59973 Canine IL-13Ralpha
c	17	877	60.3	878	22	AAS59960 Canine interleukin
c	18	877	60.3	878	22	AAS59961 Canine interleukin
c	19	842.4	57.9	1298	18	AAT86464 Human interleukin-
c	20	842.4	57.9	1298	18	AAT86464 Human interleukin-
c	21	842	57.9	1369	18	AAT95214 Nucleotide sequenc
c	22	842	57.9	1369	18	AAT95214 cDNA encoding the
c	23	842	57.9	1369	22	AAS59991 Human Interleukin-
c	24	842	57.9	1369	22	AAS59993 Human Interleukin-
c	25	842	57.9	1369	22	AAD02335 Human Interleukin
c	26	842	57.9	1369	22	AAC81416 Human IL-13 recept
c	27	839.6	57.7	1288	19	AAV04131 Human HR-1 recepto
c	28	839.6	57.7	1288	19	AAV04075 Human cytokine/pep
c	29	839.6	57.7	1288	19	AAV02295 Homo sapiens cDNA
c	30	839	57.7	1289	18	AAT96782 Human Zcytor2 cyto
c	31	787.4	54.2	1126	18	AAT96782 Celebus maceque Zc
c	32	780.4	53.7	1167	18	AAT96783 Human Zcytor2 cyto
c	33	727	50.0	1525	18	AAT95213 cDNA encoding the
c	34	727	50.0	1525	21	AAA27911 cDNA encoding IL-1
c	35	727	50.0	1525	22	AAS59990 Mouse Interleukin-
c	36	727	50.0	1525	22	AAS59992 Mouse Interleukin-
c	37	727	50.0	1525	22	AAD02334 Murine Interleukin
c	38	727	50.0	1525	22	AAC81415 Mouse IL-13 recept
c	39	712.6	49.0	951	24	AAC22980 Human soluble cyto
c	40	712.4	49.0	947	19	AAV22702 Mature interleukin
c	41	712.4	49.0	1079	19	AAV22701 Construct containi
c	42	620	42.6	620	22	AAS59958 Canine interleukin
c	43	620	42.6	620	22	AAS59959 Canine interleukin
c	44	419.4	28.8	1539	18	AAT85826 Human interleukin-
c	45	308	21.2	456	20	AAV89756 EST clone CS520.

ALIGNMENTS

RESULT 1

AAS59962 ID AAS59962 standard; cDNA; 1454 BP.

XX AC AAS59962,

XX DT 29-JAN-2002 (first entry)

XX DE Canine interleukin l3 receptor cDNA nCaIL-13Ralpha2 1454.

XX KW Dog: interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;

XX KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;

XX KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;

XX KW immune response.

XX OS Canis familiaris.

XX PN WO200177332-A2.

XX XX PD 18-OCT-2001.

XX XX PF 09-APR-2001; 2001WO-US11498.

XX XX PR 07-APR-2000; 2000US-195659P.

XX XX PR 07-APR-2000; 2000US-195874P.

XX PA (HESK-) HESKA CORP.

XX PI McCall CA, Tang L;

XX XX WPI; 2001-657172/75.

XX DR P-PSDB; AAU69135.

XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS Claim 19; Page 173-175; 221pp; English.
XX

CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13 proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
SQ Sequence 1454 BP; 491 A; 238 C; 282 G; 442 T; 1 other;

Query Match 99.9%; Score 1453; DB 22; Length 1454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggcacagagctgagttgtgctgtgattatcagacagagaggaaggtcttagagattct 60
Db 1 ggcacagagctgagttgtgctgtgattatcagacagagaggaaggtcttagagattct 60
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Db 61 aattaatgtctccaaactggagagagaaaaaagagacctgtgataattgcctatga 120
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QY 421 tggaaagaccatctattaccagaatctacattacaaagatgggtttgatcttaacaaagt 480
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Db 1201 gtatttttctgataccatttctgttctcaatatttggtaataacttgctgt 1260
QY 1261 cttttgtataagcaagggctttactgaaacgacatcttctacacaaaaaagaagcttt 1320
Db 1261 cttttgtataagcaagggctttactgaaacgacatcttctacacaaaaaagaagcttt 1320
QY 1321 tctcatcaagacacatttctgtgactcagtaacttcttcttcttcttcttcttcttctt 1380
Db 1321 tctcatcaagacacatttctgtgactcagtaacttcttcttcttcttcttcttcttctt 1380
QY 1381 atgagctctattaaactgaagcttttctcctcaaatattgataaaatcttttttaaanga 1440
Db 1381 atgagctctattaaactgaagcttttctcctcaaatattgataaaatcttttttaaanga 1440
QY 1441 aaaaaaaaaaaaaa 1454
Db 1441 aaaaaaaaaaaaaa 1454

RESULT 2
AAS59963/c
ID AAS59963 standard; cDNA; 1454 BP.
XX
AC AAS59963;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine interleukin 13 receptor cDNA nCaIL-13ralpha2 1454 complement.
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX immune response.
OS Canis familiaris.
XX

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PN WO200177332-A2.
XX
XX
PD 18-OCT-2001.
XX
XX
PF 09-APR-2001; 2001WO-US11498.
XX
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
XX
PA (HESK-) HESKA CORP.
XX
XX
PI McCall CA, Tang L;
XX
XX
DR WPI; 2001-657172/75.
XX
XX
PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX
PS Claim 19; Page 177-178; 221pp; English.
XX
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13/alpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13 mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.
XX
XX
SQ Sequence 1454 BP; 442 A; 282 C; 238 G; 491 T; 1 other:

Query Match          99.9%; Score 1453; DB 22; Length 1454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggcacgagcgtgagttgtgtgcttgattatcagacaggaaggaagctgttagattct 60
Db 1454 GGCACGAGCCTGAGTTGTGCTTGATTATCAGACAGGAGGAAGTCTTAGAGATTCT 1395

Qy 61 aattaatgtctccaaactggagaagagaaaaaagagaccctgtgataattgcctatga 120
Db 1394 AATTAATGTCTCCAAACTGGAGAAGAGAAAAAAGAGAGACCCTGTGATAATTGCCTATGA 1335

Qy 121 taattcattcttgagaaccatattattgagtgaacttcaaatcgaagtattgtaattcttgg 180
Db 1334 TAATTTCATTCTTGAGAAACCATATATTGAGTGAAACTTCAAAGATATTGAATCTTGA 1275

Qy 181 ggaatgggtttcatttcatttgatgcggatccctctatcacocctgttgttgcacagca 240
Db 1274 GGAATGGGTTTCATTTCATTGGATCGGATTCCTCTATACCCCTGCTTTGGCACAGCA 1215

Qy 241 ttggctctatgctttcctaaatgctgagataaaagttaattcctcctcaggaattttgagata 300
Db 1214 TTGGCTCTATGCTTTCAAATGCTGAGATAAAAGTTAATCCCTCCTCAGGATTTTGAGATA 1155

Qy 301 gtggaccttgatatattaggttatctctcttggcaatggcaacctccattttccgcat 360
Db 1154 GTGGACCTTGGATATTTAGGTTATCTCTTTGCAATGGCAACCTCCCAATATTTCCGGAT 1095

Qy 361 aattttaagggaatgcacataagaatatgaattaaataaccgaaacattgtagtgaaac 420
Db 1094 AATTTTAAGGAATGCACATAGAAATGAATTAATAACCGAAACATTCATGATAGTGAAC 1035

Qy 421 tggagaccatcattaccagaagatcattacaaagatgggtttgatctttaacaaagt 480

```

RESULT 3
AAS59964

ID AAS59964 standard; cDNA; 1158 BP.
 AC AAS59964;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1158.
 XX
 KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IL-13Ralpha2; Immunoglobulin heavy chain; IgG FC;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.
 XX
 OS Canis familiaris.
 XX
 PN WO200177332-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 09-APR-2001; 2001WO-US11498.
 XX
 PR 07-APR-2000; 2000US-195659P.
 PR 07-APR-2000; 2000US-195874P.
 XX
 PA (HESK-) HESKA CORP.
 PI McCall CA, Tang L;
 XX
 DR WPI; 2001-657172/75.
 XX
 PT Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 XX
 PS Claim 19; Page 178; 221pp; English.
 XX
 CC The invention concerns an isolated canine protein, preferably canine
 CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, fusion proteins between the IgG and IL-13R proteins
 CC and methods of isolating regulators of them. The regulators are useful
 CC for regulating an immune response in a canine. The proteins are useful
 CC when administered to a canine in an effective manner, are capable of
 CC developing regulatory compounds including inhibitors and activators that,
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene
 CC therapy). The present sequence encodes a protein of the invention.
 XX
 SQ Sequence 1158 BP; 380 A; 201 C; 224 G; 353 T; 0 other;

Query Match 79.6%; Score 1158; DB 22; Length 1158;
 Best Local Similarity 100.0%; Pred. No. 8.1e-261;
 Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 atggcttccattcattggatgcggattccctctatcacctcgtctgtttgcacgacattt 243
 DB 1 atggcttccattcattggatgcggattccctctatcacctcgtctgtttgcacgacattt 60
 QY 244 ggctctatgcttccaaatgctgagataaaagttaactccctccagattttgagatagtg 303
 DB 61 ggctctatgcttccaaatgctgagataaaagttaactccctccagattttgagatagtg 120
 QY 304 gacctggatattgggttatctctcttggaaatggaaacctccattatttccggataat 363
 DB 121 gacctggatattgggttatctctcttggaaatggaaacctccattatttccggataat 180
 QY 364 tttaagggaatgcacatagaataaataaataaccgaacatagtagtgaactgg 423
 DB 181 tttaagggaatgcacatagaataaataaataaccgaacatagtagtgaactgg 240

QY 424 aagaccatcattaccaagaatctcattacaaagatgggtttgatcttcaacaaggtatt 483
 DB 241 aagaccatcattaccaagaatctcattacaaagatgggtttgatcttcaacaaggtatt 300
 QY 484 gaagcaagataaaacacactcttgcagacacaaatggatcagaagttagaagt 543
 DB 301 gaagcaagataaaacacactcttgcagacacaaatggatcagaagttagaagt 360
 QY 544 tcattggcagaactacttatttggacatcacacaaagaaatcggaactaaaattcaa 603
 DB 361 tcattggcagaactacttatttggacatcacacaaagaaatcggaactaaaattcaa 420
 QY 604 gatatggactgtgtatatatacaactggcaattatttagtctgctcttggaaacctggcatg 663
 DB 421 gatatggactgtgtatatatacaactggcaattatttagtctgctcttggaaacctggcatg 480
 QY 664 ggtgtccatttggataccacaaattaccagttgttttactggtatgagggtcttgaccattca 723
 DB 481 ggtgtccatttggataccacaaattaccagttgttttactggtatgagggtcttgaccattca 540
 QY 724 gcagagtgtactgattacatcaaggttaatggaaaaaatatgggatgcagggtttccctat 783
 DB 541 gcagagtgtactgattacatcaaggttaatggaaaaaatatgggatgcagggtttccctat 600
 QY 784 ttggagtcatcagactataaagatttctacatctgtgttaattgggttcacagaatcccaag 843
 DB 601 ttggagtcatcagactataaagatttctacatctgtgttaattgggttcacagaatcccaag 660
 QY 844 cctatcagaccagctatttttatttttcagcttcaaaatatagtttaaacctatgcacacca 903
 DB 661 cctatcagaccagctatttttatttttcagcttcaaaatatagtttaaacctatgcacacca 720
 QY 904 gactaccttagtcttactgtgagaattcagagaaataaaccctgaaatggaaatgcct 963
 DB 721 gactaccttagtcttactgtgagaattcagagaaataaaccctgaaatggaaatgcct 780
 QY 964 aaaggaccattccagcccaaatgtttcatttatgaattgaattcagagatgggtact 1023
 DB 781 aaaggaccattccagcccaaatgtttcatttatgaattgaattcagagatgggtact 840
 QY 1024 acttgggtgactaccacagttgagaatgagatcacaaatcacagaacatcaaatgaaagc 1083
 DB 841 acttgggtgactaccacagttgagaatgagatcacaaatcacagaacatcaaatgaaagc 900
 QY 1084 caaaatattgctttttgtgaagaagtaagtaattattttgtctcagatgagaaatc 1143
 DB 901 caaaatattgctttttgtgaagaagtaagtaattattttgtctcagatgagaaatc 960
 QY 1144 tggagtgagtggatgatacaaatgctggaaggtgacatatggagaaaccttagta 1203
 DB 961 tggagtgagtggatgatacaaatgctggaaggtgacatatggagaaaccttagta 1020
 QY 1204 tttttctgataccatttctgtctcattatttggtaatttggtaataaactgctgctt 1263
 DB 1021 tttttctgataccatttctgtctcattatttggtaatttggtaataaactgctgctt 1080
 QY 1264 ttgtataacaaagggttttactgaaacgatcttttcacaaaaaaagaagcttttct 1323
 DB 1081 ttgtataacaaagggttttactgaaacgatcttttcacaaaaaaagaagcttttct 1140
 QY 1324 catcaagacacattctgt 1341
 DB 1141 catcaagacacattctgt 1158
 RESULT 4
 AAS59965/c
 ID AAS59965 standard; cDNA; 1158 BP.
 XX
 AC AAS59965;
 XX
 DT 29-JAN-2002 (first entry)
 XX

DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1158 complement.
 XX
 KW Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.
 XX
 OS Canis familiaris.
 XX
 PN WO200177332-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 09-APR-2001; 2001WO-US11498.
 XX
 PR 07-APR-2000; 2000US-195659P.
 PR 07-APR-2000; 2000US-195874P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 XX McCall CA, Tang L;
 PI
 XX
 DR WPI; 2001-657172/75.
 XX
 PT Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 XX
 PS Claim 19; Page 179; 221pp; English.
 XX
 CC The invention concerns an isolated canine protein, preferably canine
 CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, the fusion proteins between the IgG and IL-13R proteins
 CC and methods of isolating regulators of them. The regulators are useful
 CC for regulating an immune response in a canine. The proteins useful to
 CC develop regulatory compounds including inhibitors and activators that,
 CC when administered to a canine in an effective manner, are capable of
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene
 CC therapy). The present sequence is the reverse complement of a cDNA
 CC encoding a protein of the invention.
 XX
 SQ Sequence 1158 BP; 353 A; 224 C; 201 G; 380 T; 0 other;

Query Match 79.6%; Score 1158; DB 22; Length 1158;
 Best Local Similarity 100.0%; Pred. No. 8.le-261;
 Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 184 atggcttcattcattggatcgagatcgagatccctctatccctctgttggcagcattt 243
 DB 1158 ATGGCTTCATTTCATTTGGATCGGATTCCTCTATACCCTGCTTGTTCACACGATTT 1099
 QY 244 ggcctatgcttcaaaatcgatgataaaagttaacccctcagatgtttgagatagtg 303
 DB 1098 GGCTCTATGCTTTCAAATGCTGAGATAAAAGTTAATCTCCCTCAGGATTTTGATAGTG 1039
 QY 304 gacctggatattagggttatctctcttggcaatggcaacctccattattccggataat 363
 DB 1038 GACCTGGGATATTTAGGTTATCTCTTTGCAATGGCAACCTCCATTATTTCCGGATAAT 979
 QY 364 tttaagggaatgcacaatagaatataaattaaataaccgaaacattgatgtgaaactgg 423
 DB 978 TTTAAGGAATGCACAATAGAAATGAATTTAAATACCGAAACATTGATAGTGAATACTGG 919
 QY 424 aagaccattaccacaagaatcattacagaagatgggttgatccttaacaaggattt 483
 DB 918 AAGACCATCATTTACCAAGAATTTACATTTACAAAGATGGGTTTGATCTTTAACCAAGGTATT 859
 QY 484 gaagcaagaataaacacacattcttcgcagcacaatgcacaatggatcagaagttagaagt 543

DB 858 GAAGCAAAAGATAAACACACACTTTCGCCAGCACAAATGCACAAATGGATCAGAAGTTAGAAGT 799
 QY 544 tcatggcgagaactactctatttgagcatcaccacaaggaatcggaactaaaaattcaa 603
 DB 798 TCATGGCGAGAAATACATTATTTGGACATCACCACAGGAATCGGGAATCAAAATTCAA 739
 QY 604 gatatggactgtgtatattacaactggcaatatttagtctgtctcttggaaactggcatg 663
 DB 738 GATATGGAGTGTGTATATTTACAACATGGCAATATTTAGTGTCTTGTGGAAACCTGGCATG 679
 QY 664 ggtgtccatttggatataccaattaccagttgttttactgtgtatgaggtctggaccattca 723
 DB 678 GGTGTCCATTTTGATACCAATTTACCAGTTGTCTTACTGTATGAGGGCTTGGACCAATCA 619
 QY 724 gcagagtgtactgattacatcaaggttaatggaaaaataatggatgcaggtttccctat 783
 DB 618 GCAGAGTGTACTGATTTACATCAAGGTTAATGGAAAAAATATGGGATGCAGGTTTCCTAT 559
 QY 784 ttggagtcacagactataaagatttctacatctgtttaaagggttcacagaatcccgag 843
 DB 558 TTGGAGTCATCAGACTATAAGATTTCTACATCTGTGTAAATGGGTTCATCAGAATCCAG 499
 QY 844 cctatcagaccagctatttatttttcagcttcaaaatataagtttaaacctatgccacca 903
 DB 498 CCTATCAGACCCAGCTATTTTATTTTTCAGCTTCAAAATATAGTTAAACCTATGCCACCA 439
 QY 904 gactaccttagtctactgtgaagaattcagaggaattaaacctgaatggaatgcacgcct 963
 DB 438 GACTACTTAGTCTTACTGTGAAGAATTCAGAGGAATTAACCTGAATGGAACATGCCCT 379
 QY 964 aaaggaccttccagccaaatgtttcatttatgaattgaattcacagaggtgact 1023
 DB 378 AAAGGACCCATTCAGCCAAATGTTCATTATGAATTTGAATTCACAGAGGATGCTACT 319
 QY 1024 acttgggtgactaccagattgagaatgagatacaaaatcacagaacatacaaatgaaagc 1083
 DB 318 ACTTGGGTGACTTACCACAGTTGAGAATGAGATACAAATCACAAGAACATCAAAATGAAAGC 259
 QY 1084 caaaaattatgcttttggtaagaagtaagtaattatttattgctcagatgatgaatc 1143
 DB 258 CAAAATTTATGCTTTTGGTAGAAGTAAGTAAGTAATTTATTTGCTCAGATGATGAATC 199
 QY 1144 tggagtgtgagtgatgaacaatgctggaaggtgacatatggaaggaacacttagta 1203
 DB 198 TGGAGTGTAGTGGAGTGATGAACAATGCTGGAAAGGTGACATATGGAAGGAACCTTAGTA 139
 QY 1204 ttttttggatccatttctgttctcaatatttggtttggtaataacttgcctgctt 1263
 DB 138 TTTTCTTGTATACCATTTGCTTTGTCTCAATATTTTGTGTAATAACTTGCCTGCTT 79
 QY 1264 ttgtataagcaaggctttactgaaaacgatcttccatcacaaaaaagaagcttttct 1323
 DB 78 TTGTATAAGCAAGGGCTTTTACTGAAAACGATCTTTTCATACAAAAAAGAAGTCTTTCT 19
 QY 1324 catcaagacacattctgt 1341
 DB 18 CATCAAGACACATTCGT 1

RESULT 5

AAS59966

ID AAS59966 standard; cDNA; 1095 BP.

XX AAS59966;

XX AAS59966;

DT 29-JAN-2002 (first entry)

XX Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1095.

XX Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;

KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;

KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;

immune response.
Canis familiaris.
WO200177332-A2.
18-OCT-2001.
09-APR-2001; 2001WO-US11498.
07-APR-2000; 2000US-195659P.
07-APR-2000; 2000US-195874P.
(HESK-) HESKA CORP.
McCall CA, Tang L;
WPI; 2001-657172/75.
P-PSDB; AAU69136.
Novel isolated canine protein, preferably canine immunoglobulin G protein or canine interleukin-13 receptor protein useful for regulating immune response of an animal and for developing regulatory compounds -
Claim 19; Page 179-181; 221pp; English.
The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13 proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence encodes a protein of the invention.
Sequence 1095 BP; 370 A; 186 C; 211 G; 328 T; 0 other;

Query Match 75.3%; Score 1095; DB 22; Length 1095;
Best Local Similarity 100.0%; Pred. No. 4.1e-246;
Matches 1095; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 tctatgctttcaaatgctgagataaaagttaattctctctcctcaggaattttgagatagtgac 306
DB 1 tctatgctttcaaatgctgagataaaagttaattctctcctcaggaattttgagatagtgac 60
QY 307 cctggatatttaggtttatctctcttgcgaatggcaacctccattatttccggataatttt 366
DB 61 cctggatatttaggtttatctctcttgcgaatggcaacctccattatttccggataatttt 120
QY 367 aaggaatgcacaatagaatgaattaaataaccgaacattgtagtgaaactggaag 426
DB 121 aaggaatgcacaatagaatgaattaaataaccgaacattgtagtgaaactggaag 180
QY 427 accatcattaccagaatctacataaagatgggtttgattcttcaacaaagatttgaa 486
DB 181 accatcattaccagaatctacataaagatgggtttgattcttcaacaaagatttgaa 240
QY 487 gcaagataaaacacactcttgcagcaccaatgcacaaatggatcagaagttagaagtcca 546
DB 241 gcaagataaaacacactcttgcagcaccaatgcacaaatggatcagaagttagaagtcca 300
QY 547 tgggcagaactactatttgacatcacacaaggaatcgggaaactaaattcaagat 606
DB 301 tgggcagaactactatttgacatcacacaaggaatcgggaaactaaattcaagat 360
QY 607 atggactgtgtattacaaactggcaattatttagtctcttggaaacctggatgggt 666

DB 361 atggactgtgtattacaaactggcaattatttagtctcttggaaacctggatgggt 420
QY 667 gtcatttttgataccaattaccagttgttttactggtatgagggttgaccattcagca 726
DB 421 gtcatttttgataccaattaccagttgttttactggtatgagggttgaccattcagca 480
QY 727 gagtgtactgattacatcaaggttaattggaataaaatattggatgcaggtttccctatttg 786
DB 481 gagtgtactgattacatcaaggttaattggaataaaatattggatgcaggtttccctatttg 540
QY 787 gagtcatcagactataaagatttttcaatctctgtttaaattgggttcacagaatcccagcct 846
DB 541 gagtcatcagactataaagatttttcaatctctgtttaaattgggttcacagaatcccagcct 600
QY 847 atcagaccagctatt 906
DB 601 atcagaccagctatt 660
QY 907 taccttagtcttactgtgaagaattcagaggaattaaacctgaaatggaaatggcaatgcctaaa 966
DB 661 taccttagtcttactgtgaagaattcagaggaattaaacctgaaatggaaatggcaatgcctaaa 720
QY 967 ggaccattccagcccaaatgtttcatttgaattgaattcagaggaattggtactact 1026
DB 721 ggaccattccagcccaaatgtttcatttgaattgaattcagaggaattggtactact 780
QY 1027 tgggtgactaccacagcttgagaatgagatcacaaatcacagaacatcaaatgaaagccaa 1086
DB 781 tgggtgactaccacagcttgagaatgagatcacaaatcacagaacatcaaatgaaagccaa 840
QY 1087 aaattatgcttttttggtaagaaatgaatgaattatttttctcagatgaggaatctgg 1146
DB 841 aaattatgcttttttggtaagaaatgaatgaattatttttctcagatgaggaatctgg 900
QY 1147 agtgaatgagatgagaaatgctggaaggtgacatgacatggaagaacaccttagtattt 1206
DB 901 agtgaatgagatgagaaatgctggaaggtgacatgacatggaagaacaccttagtattt 960
QY 1207 tcttgatcaccattgcttttctcaatttttggtaatttttggtaataactgctgcttttg 1266
DB 961 tcttgatcaccattgcttttctcaatttttggtaatttttggtaataactgctgcttttg 1020
QY 1267 tataagcaaaagggttttactgaaacgacttttctacaaaaaaagaagcttttttctcat 1326
DB 1021 tataagcaaaagggttttactgaaacgacttttctacaaaaaaagaagcttttttctcat 1080
QY 1327 caagacacattctgt 1341
DB 1081 caagacacattctgt 1095
RESULT 6
AAS59967/c
ID AAS59967 standard; cDNA; 1095 BP.
XX AC AAS59967;
XX DT 29-JAN-2002 (first entry)
XX DE Canine interleukin 13 receptor cDNA nCaIL-13Ralpha2 1095 complement.
XX KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
XX KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX immune response.
XX OS Canis familiaris.
XX XX
XX PN WO200177332-A2.
XX XX
XX PD 18-OCT-2001.
XX PF 09-APR-2001; 2001WO-US11498.

[illegible]

DR P-PSDB; AAU69137.
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS Claim 19; Page 184-185; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
SQ Sequence 954 BP; 329 A; 162 C; 192 G; 271 T; 0 other;

Query Match 65.2%; Score 947.8; DB 22; Length 954;
Best Local Similarity 99.8%; Pred. No. 9, 2e-212;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 247 tctatgcttccaagtctgagataaaagttaatactctcctcaggatttgagatagtgagc 306
DB 4 tctatgcttccaagtctgagataaaagttaatactctcctcaggatttgagatagtgagc 63
QY 307 cctgcatatttaggttatctctcttgcaatggcagacccattattccggataatttt 366
DB 64 cctgcatatttaggttatctctcttgcaatggcagacccattattccggataatttt 123
QY 367 aggggaatgcacataatgaattaaataccgaacattgtagtgagaaactggag 426
DB 124 aagggaatgcacataatgaattaaataccgaacattgtagtgagaaactggag 183
QY 427 accatattaccagaatacatcattacaagaatgggttgatcttcaacaaggattgaa 486
DB 184 accatattaccagaatacatcattacaagaatgggttgatcttcaacaaggattgaa 243
QY 487 gcaagataaacaacacctctgcagcacacaaatgcacaaatggatcagaagttgaa 546
DB 244 gcaagataaacaacacctctgcagcacacaaatgcacaaatggatcagaagttgaa 303
QY 547 tgggcagaaactactatttggacatccaccagaagaatcgggaaactaaaattcaagat 606
DB 304 tgggcagaaactactatttggacatccaccagaagaatcgggaaactaaaattcaagat 363
QY 607 atggactgtgtattatacaactgggaataatttagtctgtcttggaaacctggatgggt 566
DB 364 atggactgtgtattatacaactgggaataatttagtctgtcttggaaacctggatgggt 423
QY 667 gtccatttgcaccaaataacacagttgtttactggtatgaggtctggaccattcagca 726
DB 424 gtccatttgcaccaaataacacagttgtttactggtatgaggtctggaccattcagca 483
QY 727 gaggctactgattatcatacaaggttaattggaaaaaataatggggtcagggtttccctatttg 786
DB 484 gaggctactgattatcatacaaggttaattggaaaaaataatggggtcagggtttccctatttg 543
QY 787 gaggctacagacataaagatttcacatctgtttaatgggtcagaaatcccagcct 846
DB 544 gaggctacagacataaagatttcacatctgtttaatgggtcagaaatcccagcct 603
QY 847 atcagaccagctattttattttttcagcttcaaaatacatagtttaaacctatgccacagac 906
DB 604 atcagaccagctattttattttttcagcttcaaaatacatagtttaaacctatgccacagac 663

QY 907 taccttagtcttactgtggaattcagagaaataactgaaatggaactgcctaaa 966
DB 664 taccttagtcttactgtggaattcagagaaataactgaaatggaactgcctaaa 723
QY 967 ggaccattccagccaaaatgtttcattttatgaaattgaattccacagaggtggtactact 1026
DB 724 ggaccattccagccaaaatgtttcattttatgaaattgaattccacagaggtggtactact 783
QY 1027 tgggtgactaccacagttgagaatgagatcacaaatcacagaacatcaaatgaaagccaa 1086
DB 784 tgggtgactaccacagttgagaatgagatcacaaatcacagaacatcaaatgaaagccaa 843
QY 1087 aaattatgcttttttggtaagaagtaaaagtgaattattttgtcagatgattgaaactctgg 1146
DB 844 aaattatgcttttttggtaagaagtaaaagtgaattattttgtcagatgattgaaactctgg 903
QY 1147 agtgagtgagtgatgaacaaatgcctggaaagtgacatattgaaagaaacc 1197
DB 904 agtgagtgagtgatgaacaaatgcctggaaagtgatattctggaagaaacc 954
RESULT 8
AAS59969/c
ID AAS59969 standard; cDNA; 954 BP.
XX
AC AAS59969;
XX
DT 29-JAN-2002 (first entry)
DE Canine IL-13R extracellular domain cDNA nCaIL-13Ralpha2 954 complement.
XX
KW Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW Immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.
XX
PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS Claim 19; Page 187; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence is the reverse complement of a cDNA
CC encoding a protein of the invention.

```

xx
SQ Sequence 954 BP; 271 A; 192 C; 162 G; 329 T; 0 other;

Query Match      65.2%; Score 947.8; DB 22; Length 954;
Best Local Similarity 99.8%; Pred. No. 9.2e-212;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 247 tctatgcttcaaatgctgagataaaagttaatcctctcaggattttgagatagtgac 306
Db 951 TCTATGCTTTCAAAATGCTGAGATAAAAGTTAATCTCTCTCAGGATTTTGAGATAGTGAC 892
Qy 307 cctgagatttaggttactctcttgcattgcaatgcgaacctccattattcccgataatttt 366
Db 891 CCTGGATATTTAGGTTATCTCTCTTTGGCAATGGCAACTCCCATTAATTTCCGGATAATTTT 832
Qy 367 aaggaatgcacaatagaataatgaataacacccaacattgattgataaactgggaag 426
Db 831 AAGGAATGCACAATAGATATGAATTAANAATACCGAACAATGATAGTGAAACTGGGAAG 772
Qy 427 accatcattaccaagaatctacattacaaagatgggtttgattctttaacaaaggattttaa 486
Db 771 ACCATCATTTACCAAGAACTACATTACAAAGATGGTTTGATCTTAACAAAGGTATTGAA 712
Qy 487 gcaaaagataaacacactctgcccagcacaaatgcacaaatgatacgaagttagaagttaa 546
Db 711 GCAAAGATAAACAACACTTCTGCCAGCACAAATGCACAAATGGATGCAGAAAGTTAGAAGTTCA 652
Qy 547 tgggcagaactactattgacatccacacaagaatcggaactggaactaaattcaagat 606
Db 651 TGGGCAGAAACTACTATTGACATCCACCAAGGAATCGGGAACCTAAATTCAGAT 592
Qy 607 atggactgttatattacaactggcaattatttagtctctcttggaaacctggcattgggt 666
Db 591 ATGGACTGTATATTACAACCTGGCAATATTAGTCTCTCTTGGAAACCTGGCATGGGT 532
Qy 667 gtccattttgtataccaattaccagttgtttacttggtatgagggcttgaccattcaaga 726
Db 531 GTCCATTTTGTATACCAATTTACAGTTGTTTACTGGTATGAGGGCTTGGACCATTCAGCA 472
Qy 727 gagtctactgattacataaggttaagtgaataatggaatcgaggtttccctatttg 786
Db 471 GAGTGTACTGATTACATCAGGTTAATGGAATAATATGGGATGCGAGGTTTCCCTATTTG 412
Qy 787 gagtcatcagactataagattctcacatctgtgttaattgggtcatcagaatcccgact 846
Db 411 GAGTCATCAGACTATAAGATTTCTACATCTGTGTTAATGGTCTCATCAATCCAGCCT 352
Qy 847 atcagaccagactatttatttttcagcttcaaaaatagtttaaacctatgcccacagac 906
Db 351 ATCAGACCCAGCTATTTTATTTTTCAGCTTCAAAAATATAGTTAAACCTATGCCACCAGAC 292
Qy 907 taccttagtcttactgtgaagaattcagaggaaaataaccctgaaatggaacatgctctaaa 966
Db 291 TACCTTAGTCTTACTGTGAAGAATTCAGAGGAAATTAACCTGAATGGAACATGCTCTAAA 232
Qy 967 ggaccattccagccaaagtgttcatttatgaaattgaattcacagaggttggtactact 1026
Db 231 GGACCCATTCAGCCCAATGTTTCATTTATGAAATGGAATTCACAGAGATGGTACTACT 172
Qy 1027 tgggtgactaccacagttgagaatgagatacaaaatcacaaagaacatcaaatgaaagccaa 1086
Db 171 TGGGTGACTACCACAGTTTGAGAAATGAGATACAAATCACAAAGAACATCAATGAAAGCCAA 112
Qy 1087 aaattatgcttttggtaagaagtaagtgaataattatttctcagatgagtggaatctcgg 1146
Db 111 AAATTTATGCTTTTGGTAAGAAGTAAAGTGAATATTTTATGCTCAGATGATGGAATCTGG 52
Qy 1147 agtgggtgagtgatgaacaatgctggaaagtgacatgatgaaagaaacc 1197
Db 51 AGTGAGTGGAGTGATGAACAATGCTGGAAAGGTGATATCTCTGGAAGAAACC 1
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RESULT 9
AAS59970
ID AAS59970 standard; cDNA; 1686 BP.
XX AC AAS59970;
XX 29-JAN-2002 (first entry)
XX DE Canine IL-13R/IgG-Fc fusion protein cDNA nCaIL-13Ralpha2-Fc3523 1683.
XX DOG; Interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
XX IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
XX immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
XX immune response.
XX OS Canis familiaris.
XX PN WO200177332-A2.
XX 18-OCT-2001.
XX PD 09-APR-2001; 2001WO-US11498.
XX PF 07-APR-2000; 2000US-195659P.
XX PR 07-APR-2000; 2000US-195674P.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Tang L;
XX WPI; 2001-657172/75.
XX DR P-PSDB; AAU69138.
XX PT Novel isolated canine protein, preferably canine immunoglobulin G
XX protein or canine interleukin-13 receptor protein useful for regulating
XX immune response of an animal and for developing regulatory compounds -
XX Claim 37; Page 187-190; 221pp; English.
XX The invention concerns an isolated canine protein, preferably canine
XX immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
XX receptor protein, the nucleic acids encoding them, antibodies
XX raised against them, fusion proteins between the IgG and IL-13 proteins
XX and methods of isolating regulators of them. The regulators are useful
XX for regulating an immune response in a canine. The proteins useful to
XX develop regulatory compounds including inhibitors and activators that,
XX when administered to a canine in an effective manner, are capable of
XX protecting canine from disease mediated by IL-13Ralpha or IL-13. The
XX regulators are useful for treating canine IgG (heavy and/or light chain)
XX and/or canine IL-13R mediated responses. The molecules of the invention
XX are useful to regulate the immune response of an animal (e.g. by gene
XX therapy). The present sequence encodes a protein of the invention.
XX SQ Sequence 1686 BP; 513 A; 384 C; 382 G; 407 T; 0 other;

Query Match      65.2%; Score 947.8; DB 22; Length 1686;
Best Local Similarity 99.8%; Pred. No. 1.1e-211;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 247 tctatgcttcaaatgctgagataaaagttaatcctctcaggattttgagatagtgac 306
Db 4 tctatgcttcaaatgctgagataaaagttaatcctctcaggattttgagatagtgac 63
Qy 307 cctgagatttaggttactctcttgcattgcaatgcgaacctccattattcccgataatttt 366
Db 64 cctgagatttaggttactctcttgcattgcaatgcgaacctccattattcccgataatttt 123
Qy 367 aaggaatgcacaatagaataatgaataacacccaacattgattgataaactgggaag 426
Db 124 aaggaatgcacaatagaataatgaataacacccaacattgattgataaactgggaag 183
Qy 427 accatcattaccaagaatctacattacaaagatgggtttgattctttaacaaaggattttaa 486
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Db 184 accatcattaccaagaattacattacaagaatgggttgatctttaacaaggattgaa 243
QY 487 gcaagataaaacacactcttcgcagcacacaatgcacaaatggtcagaagttagaagtcca 546
Db 244 gcaagataaaacacactcttcgcagcacacaatgcacaaatggtcagaagttagaagtcca 303
QY 547 tgggcagaacactcactatttggacatcacacacaggaatcgggaaactaaaattcaagat 606
Db 304 tgggcagaacactcactatttggacatcacacacaggaatcgggaaactaaaattcaagat 363
QY 607 atggactgtgtattatacaactggcaatatattagttctgtcttggaaacctggcatgggt 666
Db 364 atggactgtgtattatacaactggcaatatattagttctgtcttggaaacctggcatgggt 423
QY 667 gtccattttgatcaccaattaccagttgttttactgtgtatgagggcttggaccattcagca 726
Db 424 gtccattttgatcaccaattaccagttgttttactgtgtatgagggcttggaccattcagca 483
QY 727 gsgtgtactgattacatcaagggttaatggaaaaaatatgggatgcaggtttccctatttg 786
Db 484 gsgtgtactgattacatcaagggttaatggaaaaaatatgggatgcaggtttccctatttg 543
QY 787 gsgtcatcagacataaaagattctacatctgtgttaatgggtcatcagaatccccagcct 846
Db 544 gsgtcatcagacataaaagattctacatctgtgttaatgggtcatcagaatccccagcct 603
QY 847 atcaaccacagctattttatttttcagcttcaaaatatattgattaaacctatgccacagac 906
Db 604 atcaaccacagctattttatttttcagcttcaaaatatattgattaaacctatgccacagac 663
QY 907 taccttagtcttactgtggaattcagaggaaattaaacctgaaatggaacatgcctaaa 966
Db 664 taccttagtcttactgtggaattcagaggaaattaaacctgaaatggaacatgcctaaa 723
QY 967 gaaccattcccgccaaatgtttcatttgaattgaattgaattcagagaggtggtactact 1026
Db 724 gaaccattcccgccaaatgtttcatttgaattgaattgaattcagagaggtggtactact 783
QY 1027 tgggtgactaccacagtttgagaatgagatacaaaatcacagaacatcaaatgaagccaa 1086
Db 784 tgggtgactaccacagtttgagaatgagatacaaaatcacagaacatcaaatgaagccaa 843
QY 1087 aaattatgctttttgtggaagtaaaagtgaatatttattgtctcagatgatggaactgg 1146
Db 844 aaattatgctttttgtggaagtaaaagtgaatatttattgtctcagatgatggaactgg 903
QY 1147 agtgagtgagtgatgaacaaatgctggaaaagtgacatatgaaaggaaacc 1197
Db 904 agtgagtgagtgatgaacaaatgctggaaaagtgatctatctggaaggaaacc 954
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RESULT 10
AAS59971/c
ID AAS59971 standard; cDNA; 1686 BP.
XX
AC AAS59971;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine IL-13Ralpha2/IgG-Fc fusion protein cDNA reverse complement.
XX
KW Dog; Interleukin-13 receptor alpha1; Interleukin-13 receptor alpha2;
IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW Immunoglobulin light chain; lambda; ss; Immunosuppressive; gene therapy;
KW Immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
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PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.
XX
Novel isolated canine protein, preferably canine immunoglobulin G
protein or canine interleukin-13 receptor protein useful for regulating
immune response of an animal and for developing regulatory compounds -
XX
Example 4; Page 193-194; 221pp; English.
PS
XX
The invention concerns an isolated canine protein, preferably canine
immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
receptor protein, the nucleic acids encoding them, antibodies
raised against them, fusion proteins between the IgG and IL-13R proteins
and methods of isolating regulators of them. The regulators are useful
for regulating an immune response in a canine. The proteins are useful
to develop regulatory compounds including inhibitors and activators that,
when administered to a canine in an effective manner, are capable of
protecting canine from disease mediated by IL-13Ralpha or IL-13. The
regulators are useful for treating canine IgG (heavy and/or light chain)
and/or canine IL-13R mediated responses. The molecules of the invention
are useful to regulate the immune response of an animal (e.g. by gene
therapy). The present sequence is the reverse complement of a cDNA
encoding a protein of the invention.
XX
SQ Sequence 1686 BP; 407 A; 382 C; 384 G; 513 T; 0 other;
XX
Query Match 65.2%; Score 947.8; DB 22; Length 1686;
Best Local Similarity 99.8%; Pred. No. 1.1e-211;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 247 tctatgtcttcaaaagtgcagataaaaagtaactcctcctcagattttgagatagtgagac 306
Db 1683 TCTATGCTTTCAAAATGCTGAGATAAAAGTTAATCTCTCCAGGATTTTGAGATAGTGGAC 1624
QY 307 cctggtatattagggttatctctcttgcgaatggcaacctccattatttcgggataatttt 366
Db 1623 CTGGATATTAGGTATTCTCTTTGCAATGGCAACCTCCATTTATTCGGGATAATTTT 1564
QY 367 aagggaatgcacaatagaatatgaattaaaataccgaacattgatgtgaaacctggaag 426
Db 1563 AAGGAATGCACAATAGATATGAATTAATAATACCGAAACATTCATAGTGAACCTGGAAG 1504
QY 427 accatcattaccaagaattacattacaagaatgggttttgatctttaacaaggatttga 486
Db 1503 ACCATCATTTACCAAGAATCTACATTACAAAAGATGGGTGTGATCTTTAAACAAGGTATTGAA 1444
QY 487 gcaagataaaacacacactctgcagcacacaatgcacaaatggatcagaagttagaagtcca 546
Db 1443 GCAAGATAAAACACACTTCTGCCAGCACAAATGCACAAATGGATCAGACGTTAGAGTTCA 1384
QY 547 tgggcagaacactcactatttggacatcacacacagaagaaatcgggaaactaaaattcaagat 606
Db 1383 TGGGGCAAAACTACTATTATGGACATCACCACAAAGGAAATCGGGAAACTAAAATTCAGAT 1324
QY 607 atggactgtgtattatacaactggcaatatattagttctgtcttggaaacctggcatgggt 666
Db 1323 ATGGACTGTGTATATTACAACTGGCAATATTTAGTCTGTCTCTTGGAAACCTGGCATGGGT 1264
QY 667 gtccattttgatcaccaattaccagttgttttactgtgtatgagggcttggaccattcagca 726
Db 1263 GTCCATTTTGATACCAATTTACCAGTTGTTTACTGGTATGAGGGCTTGGACCATTCAGCA 1204
QY 727 gsgtgtactgtattacatcaaggttaatgaaaaaatatgsggtatggaggtttccctatttg 786
|||||
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Db 1203 GAGTGACTGATTACATCAAGGTTAATGGAATAATATGGGATGCGAGGTTCCCTATTG 1144
Qy 787 gagtcatcagactataaagatttctacatctgtgttaaggggtcaccagatccagcct 846
|||||
Db 1143 GAGTCATCAGACTATAAGATTCTACATCTGTGTTAATGGGTCATCAGAAATCCAGCCT 1084
Qy 847 atcagaccagctatttttttccagcttcaaaatgatgtttaaactatgccaccagac 906
|||||
Db 1083 ATCAGACCCAGCTATTTTATTTTTCAGCTCAAAATATATGTTAAACCTATGCCACCAGAC 1024
Qy 907 taccttagcttactgtgaagaattcagaggaatttaacactgaattgaacatgctctaa 966
|||||
Db 1023 TACCTTAGTCTTACTGTGAAGAAATTCAGAGGAATTTAACTGAATGGAACATGCCATAA 964
Qy 967 gaccattccagccaaatgtttcatttgaattgaattcagagatggttactact 1026
Db 963 GCACCCATCCAGCCAAATGTTTCATTTATGAATGAATTCACAGAGATGTTACTACT 904
Qy 1027 tgggtgactacacacaggttgagaatgagatcacaaatcacagaacatcaaatgaaagccaa 1086
Db 903 TGGGTGACTTACCACAGTTGAGAAATGAGATPACAAATCACAGAATCAAAATGAAAGCCAA 844
Qy 1087 aaattatgcttttttggtaagaagtaaaagtgaatatatttattgctcagatgatgaaatctgg 1146
|||||
Db 843 AAATTATGCTTTTGGTAAGAAGTAAGTGAATATATTTATGCTCAGATGATGAATCTGG 784
Qy 1147 agtgagtggagtgaacaatgctggaaaggtgacatatggaaggaacc 1197
|||||
Db 783 AGTGAGTGGAGTGATGAACAATGCTGGAAAGGTGATATCTGGAAGGAAC 733

RESULT 11

ID AAS59976
XX AAS59976 standard; cDNA; 1686 BP.
AC AAS59976;
XX
Dl 29-JAN-2002 (first entry)
Dl
DE Canine IL-13R/IgG-Fc fusion protein cDNA nCaIL-13Ralpha2-Fc-B8 1683.
XX
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
PD
PF 09-APR-2001; 2001WO-US11498.
PF
XX
PR 07-APR-2000; 2000US-195659P.
PR
XX 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
XX WPI; 2001-657172/75.
DR P-PSDB; AAU69141.
XX
XX Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX Claim 37; Page 207-210; 221pp; English.
PS
XX
CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies

CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence encodes a protein of the invention.
XX
SQ Sequence 1686 BP; 512 A; 388 C; 379 G; 407 T; 0 other;

Query Match 65.2%; Score 947.8; DB 22; Length 1686;
Best Local Similarity 99.8%; Pred. No. 1.1e-211;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 247 tctatgcttcaaaatgctgagataaaagttaatcctcctcagagattttgagatagtcgac 306
Db 4 tctatgcttcaaaatgctgagataaaagttaatcctcctcagagattttgagatagtcgac 63
Qy 307 cctggaatttaggttatctctcttgcgaatggcaacctccattatttccggataatttt 366
Db 64 cctggataatttaggttatctctcttgcgaatggcaacctccattatttccggataatttt 123
Qy 367 aaggaatgcacaatagaatataatgaattaaataccgaacattgatagtgaactggaag 426
Db 124 aaggaatgcacaatagaatataatgaattaaataccgaacattgatagtgaactggaag 183
Qy 427 accatattaccaagaatctacattacaagaatgggtttagtcttacaagaagtattgaa 486
Db 184 accatattaccaagaatctacattacaagaatgggtttagtcttacaagaagtattgaa 243
Qy 487 gcaagataaaacacacttctgcagcacaaatgcacaaatggatcagaagttagaattca 546
Db 244 gcaagataaaacacacttctgcagcacaaatgcacaaatggatcagaagttagaattca 303
Qy 547 tgggcagaactacttattggacatcaccaaggaatcgggaaactaaaatccaagat 606
Db 304 tgggcagaactacttattggacatcaccaaggaatcgggaaactaaaatccaagat 363
Qy 607 atggactgtgtatattacaactggcgaatatttagtctgtctcttggaaacctggcattg 666
Db 364 atggactgtgtatattacaactggcgaatatttagtctgtctcttggaaacctggcattg 423
Qy 667 gtccatttgataccaattaccagttgttttactggtatgagggttgaccattcagca 726
Db 424 gtccatttgataccaattaccagttgttttactggtatgagggttgaccattcagca 483
Qy 727 gagtgtactgattacatcaagggttaatggaaaaaataatggatgcagggtttccctatttg 786
Db 484 gagtgtactgattacatcaagggttaatggaaaaaataatggatgcagggtttccctatttg 543
Qy 787 gagtcatcagactataaagatttctacatctgtgttaatgggttcacagaatccccagcct 846
Db 544 gagtcatcagactataaagatttctacatctgtgttaatgggttcacagaatccccagcct 603
Qy 847 atcagaccagctatttttatttttccagcttcaaaaatatagttaaaacctatgccaccagac 906
Db 604 atcagaccagctatttttatttttccagcttcaaaaatatagttaaaacctatgccaccagac 663
Qy 907 taccttagtcttactgtgaagaattcagaggaattaaacctgaatggaaatgacctaa 966
Db 664 taccttagtcttactgtgaagaattcagaggaattaaacctgaatggaaatgacctaa 723
Qy 967 gaccattccagccaaatgtttcatttgaattgaattcagagatggttactact 1026
Db 724 gaccattccagccaaatgtttcatttgaattgaattcagagatggttactact 783
Qy 1027 tgggtgactacacaggttgagaatgagatcacaaatcacagaacatcaaatgaaagccaa 1086
Db 784 tgggtgactacacaggttgagaatgagatcacaaatcacagaacatcaaatgaaagccaa 843

QY 1087 aaattatgtcttttgtaagaagtaaaagtgaatattattattgtcagatgatgaaactgg 1146
 |||||
 Db 844 aaattatgtcttttgtaagaagtaaaagtgaatattattattgtcagatgatgaaactgg 903
 |||||
 QY 1147 agtgaatgagtgatgaacaactgctggaagtgacatatggaagaaaacc 1197
 |||||
 Db 904 agtgaatgagtgatgaacaactgctggaagtgacatatggaagaaaacc 954
 |||||

RESULT 12
 AAS59977/c
 ID AAS59977 standard; cDNA; 1686 BP.
 XX
 AC AAS59977;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Canine IL-13Ralpha2/IgG-Fc fusion protein cDNA reverse complement #4.
 XX
 KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
 KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
 KW immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
 KW immune response.
 XX
 OS Canis familiaris.
 XX
 PN WO200177332-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 09-APR-2001; 2001WO-US11498.
 XX
 PR 07-APR-2000; 2000US-195659P.
 PR 07-APR-2000; 2000US-195874P.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI McCall CA, Tang L;
 XX
 DR WPI; 2001-657172/75.
 XX
 XX Novel isolated canine protein, preferably canine immunoglobulin G
 PT protein or canine interleukin-13 receptor protein useful for regulating
 PT immune response of an animal and for developing regulatory compounds -
 XX
 PS Claim 37; Page 212-213; 221pp; English.
 XX
 CC The invention concerns an isolated canine protein, preferably canine
 CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
 CC receptor protein, the nucleic acids encoding them, antibodies
 CC raised against them, fusion proteins between the IgG and IL-13 proteins
 CC and methods of isolating regulators of them. The regulators are useful
 CC for regulating an immune response in a canine. The proteins useful to
 CC develop regulatory compounds including inhibitors and activators that,
 CC when administered to a canine in an effective manner, are capable of
 CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
 CC regulators are useful for treating canine IgG (heavy and/or light chain)
 CC and/or canine IL-13R mediated responses. The molecules of the invention
 CC are useful to regulate the immune response of an animal (e.g. by gene
 CC therapy). The present sequence is the reverse complement of a cDNA
 CC encoding a protein of the invention.
 XX
 SQ Sequence 1686 BP; 407 A; 379 C; 388 G; 512 T; 0 other;

Query Match 65.2%; Score 947.8; DB 22; Length 1686;
 Best Local Similarity 99.8%; Pred. No. 1.1e-211;
 Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 247 tctatgtcttcaaaagtctgagataaaaagttaactctctccacaggattttgagatagtgac 306
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 Db 1683 TCTATGCTTTCAATGCTGAGATAAAAGTTAATCTCTCCACAGGATTTTGAGATAGTGGAC 1624
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QY 307 cctggatattagggttatctctcttgcgaatgcaacccctcattatttccggataatttt 366
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 QY 367 agggaaatgcacaatagaatatgaattaaaataccgaaacattgatgtaaaactggaag 426
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 QY 427 accatcattaccaagaatctacattcaaaagatgggtttgatctcttaaaaaagtattgaa 486
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 Db 1503 ACCATCATTTACCAAGAATCTACATTTACAAAGATGGGTTTGATCTTAACAAAGGATTGAA 1444
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 QY 487 gcaaaagataaaacacactctgccagcacaaatgcacaaatggatcagaagttaaaagtcca 546
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 Db 1443 GCAAAAGATAAACACACTCTGCCAGCACAAATGCACAAATGGATCAGAAGTTAGAAGTTCA 1384
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 QY 547 tggcggaactacttatttggacatcaccacaaggaaaatcgggaaaactaaaaattcaaat 606
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 QY 607 atggactgtgtattacaaactggcaatatttagtctgtctctcttgaaaactggcatgggt 666
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 Db 1323 ATGGACTGTGTATATTACAACCTGGCAATATTAGTCTGCTCTTTGGAAACCTGGCATGGGT 1364
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 QY 667 gtccatttggataccaattaccagttgttttactgtgtatgagggttgaccattcagca 726
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 Db 1263 GTCCATTTTGATACCAATTTACCAGTTGTTTACTGTGTATGAGGGCTTGGACCATTCAGCA 1204
 |||||
 QY 727 gagtgactgattacatcaagggttaatggaaaaaaatgggatggcaggtttccctatttg 786
 |||||
 Db 1203 GAGTGTACTGATTACATCAAGGTTAATGGAAAAAATATGGGATGCAGGTTTCCTATTTC 1144
 |||||
 QY 787 gagtcatcagactataaaagatttctacatctgtgttaatgggttcacagaatccccagcct 846
 |||||
 Db 1143 GAGTCATCAGACTATAAAGATTTTCTACATCTGTGTAAATGGGTCTATCAGAAATCCCAGCCT 1084
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 QY 847 atcagacccagctatttttactgttcagcttcaaaatatagtttaaacctatgccaccagac 906
 |||||
 Db 1083 ATCAGACCCAGCTATTTTATTTTTCAGCTTCAAAATATAGTTAAACCTATGCCACCAGAC 1024
 |||||
 QY 907 taccctagttactgtgaagaattcagaggaaaattaaacctgaaatggacaatgcctaaa 966
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 Db 1023 TACCTTAGTCTTACTGTGAAGAAATTCAGAGGAAATTAACCTGAAATGGAACATGCCTAAA 964
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 QY 967 ggaaccattccagccaaaatggttcatttataatgaattgaattcacagagatggctact 1026
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 Db 963 GGACCCCATTTCCAGCCAAAATGTTTCATTTATGAAATTTGAATTCACAGAGGATGGTACTACT 904
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 QY 1027 tgggtgactaccacagttgagaatgagatacaaaatcacagaacatcaaaatgaaagccaa 1086
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 QY 1087 aaattatgtcttttgggaagaagtaaaagtgaatattatttgcagatgatgaaactgg 1146
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 QY 1147 agtgaatgagtgatgaacaactgctggaagtgacatatgacatatgaaagaaaacc 1197
 |||||
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 |||||

RESULT 13
 AAS59974
 ID AAS59974 standard; cDNA; 1692 BP.
 XX
 AC AAS59974;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Canine IL-13R/IgG-Fc fusion protein cDNA nCaIL-13Ralpha2-Fc-B9 1689.
 XX Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
 KW

Novel isolated canine protein, preferably canine immunoglobulin G protein or canine interleukin-13 receptor protein useful for regulating immune response of an animal and for developing regulatory compounds - Example 4; Page 206; 221pp; English.

The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13R proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence is the reverse complement of a cDNA encoding a protein of the invention.

Sequence 1692 BP; 413 A; 385 C; 376 G; 518 T; 0 Other;

Query Match 65.2%; Score 947.8; DB 22; Length 1692;
Best Local Similarity 99.8%; Pred. No. 1.1e-211;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1689 TCTATGCTTTCAAAATGCTGAGATAAAAGTTAATCTCTTCAGGATTTTGAGATAGTGAC 1630
|||||
QY 307 cctggatatttaggtttatctcttgcgaatggcaacctccattattccgataatttt 366
|||||
DB 1629 CTGGATATTAGGTATGCTCTCTTGGCAATGGCAACCTCCCATTTATTCGGATATATTTT 1570
|||||
QY 367 agggatgcacaatagaatgaattaaataatccgaaacattgtagtgaaacctgggaag 426
|||||
DB 1569 AAGGAATGCACAATAGAATATGAATTAATAATACCGAAACATTGATAGTGAAAGTGAAG 1510
|||||
QY 427 acctattaccagaatctacatacaagaatgggttttgattcttaacaaaggatttga 486
|||||
DB 1509 ACCATCATTTACCAAGAATCTACATTACAAAGATGGGTTTGATCTTTAACAAAGGTATTGAA 1450
|||||
QY 487 gcaagataaacaacactcttgcagcacacaatgcacaaatggatcagaagttagaagtcca 546
|||||
DB 1449 GCAAGATAAACACACTTCTGCCAGCACAAATGCACAAATGGATCAGAGTTAGAACTTCA 1390
|||||
QY 547 tgggcagaactactatttggacatcaccacaagaaatcgggaaactaaataatccaagat 606
|||||
DB 1389 TGGGCGAAGAACTACTATTGGGACATCACCACAAGGAAATCGGGAACTAAAAATTCAGAT 1330
|||||
QY 607 atggactgttatatacaactggcaattatttagtctgctcttgaaacctggcatgggt 666
|||||
DB 1329 ATGGACTGTGTATATACAACTTGGCAATATTTAGTCTGCTCTTGGAAACCTGGCATGGGT 1270
|||||
QY 667 gtccattttgataccaattaccagttgttttacttggtatgagggcttggaccatttcagca 726
|||||
DB 1269 GTCCATTTGTATACCAATTAACAGTTGTTTACTGGTATGAGGGCTTGACCACTTCAGCA 1210
|||||
QY 727 gaggttactgatacatcaaggttaattggaaaaataatggggtcaggtttccctatttgg 786
|||||
DB 1209 GAGTGTACTGATTACATCAAGGTTAATGGAATAATATGGGATGAGGTTTCCCTATTTTC 1150
|||||
QY 787 gaggatcagactataaagattttcatctctgtttaattggttcacagaatcccagcgt 846
|||||
DB 1149 GAGTCATCAGACTATAAAGATTTCACATCTGTGTATATGGGTCTACAGAAATCCCAAGCCT 1090
|||||
QY 847 atcagaccagctattttatttttcagcttcaaaataatagtttaaacctatgcacacagac 906
|||||
DB 1089 ATCAGACCCAGCTATTTTATTTTTCAGCTTCAAAATATAGTTAAACCTATGCCACAGAC 1030
|||||
QY 907 taccctagtcttactgtgaagaattcagaggaaataaacctgaaatggaacatgctctaaa 966
|||||

|||||
Db 1029 TACCITAGTCTTACTGCTGAAGAATTCAGAGGAAATTAACCTGAAATGGAACATGCCCTAAA 970
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QY 967 ggaaccttcacagcgaatggtttcatttgaattgaattcacagagagatggtactact 1026
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QY 1027 tgggtgactaccacagttgagaatgagatacaaatcacagaacatcaaatgaaagccaa 1086
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Db 909 TGGGTGACTTACCACAGTTGAGATGAGATACAAATCACAGAACATCAATGAAGCCCAA 850
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QY 1087 aaattatgcttttggtaagaagtaaaagtgaattatttctcagatgatggaattctgg 1146
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Db 849 AAATATATGCTTTTGGTGAAGAAGTAAAGTGATATTTATTTGCTCAGATCATGGAATCTGG 790
|||||
QY 1147 agtggatgagatgatacaaatgctggaaagtgacatatggaagaaacc 1197
|||||
Db 789 ACTGAGTGGAGTGATGAACAATGCTGAAAGGTGATATCTGGAAGGAAACC 739
|||||

RESULT 15
AAS59972
ID AAS59972 standard; cDNA; 1698 BP.
XX
AC AAS59972;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine IL-13R/IgG-Fc fusion protein cDNA nCaIL-13Ralpha2-Fc4325 1695.
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
immunoglobulin light chain; lambda; ss; immunosuppressive; gene therapy;
immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.
DR P-PSDB; AAU69139.
DR
XX
PT Novel isolated canine protein, preferably canine immunoglobulin G protein or canine interleukin-13 receptor protein useful for regulating immune response of an animal and for developing regulatory compounds -
PT
PS Claim 37; Page 194-197; 221pp; English.
XX
CC The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13R proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence encodes a protein of the invention.

Query Match	65.2%	Score 947.8;	DB 22;	Length 1698;
Best Local Similarity	99.8%	Pred. No. 1.1e-211;		
Matches 949;	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;

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Qy	307	cctggatataggattatctctcttggcaatggcaacctccattatttcccgataatttt	366
Db	64	cctggatataggattatctctcttggcaatggcaacctccattatttcccgataatttt	123
Qy	367	aaggaaatgcacaaatagaaataagattaaaaatcccgaaacattgtatgtaaaaactgggaag	426
Db	124	aaggaaatgcacaaatagaaataagattaaaaatcccgaaacattgtatgtaaaaactgggaag	183
Qy	427	acctcattaccagaatactacatatcaaaaagatgggtttgtactcttaacaaagggtattgaa	486
Db	184	acctcattaccagaatactacatatcaaaaagatgggtttgtactcttaacaaagggtattgaa	243
Qy	487	gcaagataaacacacactctccagcacaaatgcacaaatgatcagaagttagaagtcca	546
Db	244	gcaagataaacacacactctccagcacaaatgcacaaatgatcagaagttagaagtcca	303
Qy	547	tgggcagaaaactacttattggacatcacccaaagaaatcgggaaactaaaattccaagt	606
Db	304	tgggcagaaaactacttattggacatcacccaaagaaatcgggaaactaaaattccaagt	363
Qy	607	atggaactgtgtatatatacaactggcaatatttagtctgtctcttgaaaacctgggaatgggt	666
Db	364	atggaactgtgtatatatacaactggcaatatttagtctgtctcttgaaaacctgggaatgggt	423
Qy	667	gtccattttgatccaaattaccagttgttttacttgggtatagggtctggaccattcaaca	726
Db	424	gtccattttgatccaaattaccagttgttttacttgggtatagggtctggaccattcaaca	483
Qy	727	gagtgactgattacatacaagtttaattggaaaaaatatggaatgcaggttttccctatttg	786
Db	484	gagtgactgattacatacaagtttaattggaaaaaatatggaatgcaggttttccctatttg	543
Qy	787	gagtcataagactataaagatttctacatctgtgttaattgggtctatcagaatccccagct	846
Db	544	gagtcataagactataaagatttctacatctgtgttaattgggtctatcagaatccccagct	603
Qy	847	atcagaccagctattttatttttcagcttccaaatatagtttaacctatgccaccagac	906
Db	604	atcagaccagctattttatttttcagcttccaaatatagtttaacctatgccaccagac	663
Qy	907	taccttagtcttactgtgaagaattccagagaaataaacctgaaatggaacatgacctaaa	966
Db	664	taccttagtcttactgtgaagaattccagagaaataaacctgaaatggaacatgacctaaa	723
Qy	967	ggaccattccagccaaatgttttcatttatgaaattgaaatccacagagatggttactact	1026
Db	724	ggaccattccagccaaatgttttcatttatgaaattgaaatccacagagatggttactact	783
Qy	1027	tgggtgactaccagttgaaatgagatacaaatcacaagaacatcaaatgaaagccaa	1086
Db	784	tgggtgactaccagttgaaatgagatacaaatcacaagaacatcaaatgaaagccaa	843
Qy	1087	aaattatgcttttttggttaagaagtaaaagtgaatatattattgtctcagatgtaggaaatctgg	1146
Db	844	aaattatgcttttttggttaagaagtaaaagtgaatatattattgtctcagatgtaggaaatctgg	903
Qy	1147	agtgagtggaatgatgaacaatgctggaagggtgacatatggaaggaaacc	1197
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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(without alignments)
5319.159 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
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- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_hgt_hum.*
- 31: em_hgt_inv.*
- 32: em_hgt_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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RESULT	1	LOCUS	AF314533	1454 bp	mrna	linear	MAM 16-OCT-2001
DEFINITION	Canis familiaris Interleukin 13 receptor alpha chain 2 (IL13Ra2)	AF314533	1454 bp	mrna	linear	MAM 16-OCT-2001	
ACCESSION	AF314533	AF314533	1454 bp	mrna	linear	MAM 16-OCT-2001	
VERSION	AF314533.1	AF314533.1	1454 bp	mrna	linear	MAM 16-OCT-2001	
KEYWORDS	Canis familiaris	Canis familiaris	1454 bp	mrna	linear	MAM 16-OCT-2001	
SOURCE	dog.	dog.	1454 bp	mrna	linear	MAM 16-OCT-2001	
ORGANISM	Canis familiaris	Canis familiaris	1454 bp	mrna	linear	MAM 16-OCT-2001	
REFERENCE	1 (bases 1 to 1454)	1 (bases 1 to 1454)	1454 bp	mrna	linear	MAM 16-OCT-2001	
AUTHORS	Tang, L.	Tang, L.	1454 bp	mrna	linear	MAM 16-OCT-2001	
TITLE	Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and alpha2) cDNAs and detection of corresponding mRNAs in canine tissues	Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and alpha2) cDNAs and detection of corresponding mRNAs in canine tissues	1454 bp	mrna	linear	MAM 16-OCT-2001	
JOURNAL	Vet. Immunol. Immunopathol. 79 (3-4), 181-195 (2001)	Vet. Immunol. Immunopathol. 79 (3-4), 181-195 (2001)	1454 bp	mrna	linear	MAM 16-OCT-2001	
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REFERENCE	2 (bases 1 to 1454)	2 (bases 1 to 1454)	1454 bp	mrna	linear	MAM 16-OCT-2001	
AUTHORS	Tang, L.	Tang, L.	1454 bp	mrna	linear	MAM 16-OCT-2001	
TITLE	Direct Submission	Direct Submission	1454 bp	mrna	linear	MAM 16-OCT-2001	

ALIGNMENTS

JOURNAL Submitted (18-OCT-2000) Allergy and Immunology, Heska Corporation,
1613 Prospect Parkway, Fort Collins, CO 80525, USA
FEATURES
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SQIPRPSFYFOLQNIWKPMPPDYLSTLVKNSERINLKNWMPKPIPAKCFIYIEFT
EDGTTWVTTTVEINQITRTSNESOKLCLFLVRSKVNLYCSDDGITWSWSBOCWKGD
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1345. .1454
3'UTR /gene="IL13Ra2"
BASE COUNT 491 a 238 c 282 g 442 t 1 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.2e-284;
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DB 301 GTGGACCTGGATATTTAGGTATCTCTCTTTGCAATGGCAACCTCCCATTTATTTCCGGAT 360
QY 361 aatttaagggaatcacatagaatatgaattaaataaccgaacacattgattgataaac 420
DB 361 AATTTTAAGGAATGCACAATAGAATATAAATAACCAATACCAATGATGATGATAAAC 420
QY 421 tggagaaccattaccacagaactctacattacaaagatgggtttgtatttaacaaaggt 480
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KEYWORDS
SOURCE dog.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)

AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 60 18-OCT-2001;
Heska Corporation (US)
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DEFINITION Sequence 62 from Patent WO0177332.
ACCESSION AX280327
VERSION AX280327.1 GI:16607705
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
receptors
JOURNAL Patent: WO 0177332-A 62 18-OCT-2001;

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AUTHORS	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.								
TITLE	1 (sites)								
JOURNAL	Mccall,C.A. and Tang,L.								
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DEFINITION Sequence 64 from Patent WO0177332.
ACCESSION AX280329
VERSION AX280329.1 GI:16607707
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine 19g and canine 11-13
receptors
JOURNAL Patent: WO 0177332-A 64 18-OCT-2001;
Heska Corporation (US)
FEATURES
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Qy 724 gcagagtgactgattacatcaaggttaagtgaataatgaggttgcaggtttccctcat 783
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QY	784	ttggagtcacagactataaaatcttacatctgtgttaattgggtcatcagaatccag	843
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Db	498	CCTATCAGACCCAGCTATTTTATTTTTCAGCTCAAAATATAGTTAAACCTATGCCACCA	439
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QY	1084	caaaatctatgcttttggtaagaagttaaagtgaatatatttattgctcagatggaatc	1143
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QY	1144	tggagtggagtgatgaacactgctgggaagtgacatatggaaggaaacaccttagta	1203
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QY	1204	ttttcttgataccattgcttttctgctcaatatatttggtttggttaataacttgcctgctt	1263
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LOCUS	AX280330	1095 bp	DNA linear PAT 02-NOV-2001
DEFINITION	Sequence	65 from Patent WO0177332.	
ACCESSION	AX280330		
VERSION	AX280330.1	GI:16607708	
KEYWORDS			
SOURCE	dog.		
ORGANISM	Canis familiaris		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
REFERENCE	1 (sites)		
AUTHORS	Mccall,C.A. and Tang,L.		
TITLE	Compositions and methods related to canine igg and canine il-13		
JOURNAL	receptors		
	Patent: WO 0177332-A 65 18-OCT-2001;		
FEATURES	Heska Corporation (US)		
source	Location/Qualifiers		
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	ECTDYIKVKNKMCRRPYLESSDYKDFYICVNGSSSQPIRPSYFFIQLQNIYKPHP		
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BASE COUNT		370 a	186 c	211 g	328 t	NESOKLCLVRSKNVIYCSDDGIWSEWSDEOCWKDIWKETLVFFLIPFAFVSIFVLV ITCILLYKQALLAKTIPIHTKKEVFSHODTFC"	
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Best Local Similarity		100.0%		Pred. No. 6.8e-212;			
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QY	367	aaggaa	tg	cacaat	tagaata	tgaatt	aaaaatccgaacattgtagtga
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RESULT 7
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DEFINITION Sequence 67 from Patent WO0177332.
ACCESSION AX280332
VERSION AX280332.1 GI:16607710
KEYWORDS
SOURCE
  dog.
ORGANISM
  Canis familiaris
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
  1 (sites)
AUTHORS
  McCall,C.A. and Tang,L.
TITLE
  Compositions and methods related to canine igg and canine il-13
JOURNAL
  Patent: WO 0177332-A 67 18-OCT-2001;
  Heska Corporation (US)
  Location/Qualifiers
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Query Match 75.3%; Score 1095; DB 6; Length 1095;
Best Local Similarity 100.0%; Pred. No. 6.8e-212;
Matches 1095; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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LOCUS Sequence 68 from Patent WO0177332.
DEFINITION
ACCESSION AX280333
VERSION AX280333.1 GI:16607711
KEYWORDS
  dog.
SOURCE
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
  1 (sites)
AUTHORS
  McCall,C.A. and Tang,L.
TITLE
  Compositions and methods related to canine igg and canine il-13
  receptors
  Patent: WO 0177332-A 68 18-OCT-2001;
  Heska Corporation (US)
  Location/Qualifiers
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Qy	607	atggactgtgtattacaaactggcaatatattagctctctcttggaaacctggcatgggt	666		
Db	364	ATGGACTGTGTATATTACAACTGGCAATATTTTGTCTCTCTTGGAACTTGGCATGGGT	423		
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Db	424	GTCCATTTTGTATACCAATTTACCAGTTGTCTTACTGGTATGAGGGCTTGGACCATTCAGCA	483		
Qy	727	gagtgactgatacatcaaatcaaggttaataaggaaaaatatgggagtgaggtttccctatttg	786		
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Qy	787	gagtcacagactataaagatttccatctgtgttaattgggtcattcagaatccccagct	846		
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Qy	847	atcagaccacagctattttatttttcagcttcaaaatagtttaaaccttatgcaccagac	906		
Db	604	ATCAGACCCAGCTATTATTATTTTTCAGCTTCAAAATATAGTTAAACCTATATGCCACAGAC	663		
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ACCESSION	AX280335				
VERSION	AX280335.1	GI:16607713			
KEYWORDS					
SOURCE	dog,				
ORGANISM	Canis familiaris				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
TITLE	1 (sites)				
JOURNAL	McCall,C.A. and Tang,L.				
FEATURES	Compositions and methods related to canine igg and canine il-13				
source	receptors				
BASE COUNT	Patent: WO 0177332-A 70 18-OCT-2001;				
ORIGIN	Heska Corporation (US)				
	Location/Qualifiers				
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Best Local Similarity	99.8%;	Pred. No. 4.3e-182;			
Matches 949;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
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Qy	547	tggcgagaactcaattatttggacatcaccaagaagaatcggaactaaataccaagat	606		
Db	651	TGGCGAGAAACTACTTTTGGACATCACCAAGGAATTCGGGAAACTTAAATATTCAGAT	592		
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (sites)
Mccall,C.A. and Tang,L.
Compositions and methods related to canine igg and canine il-13
receptors
Patent: WO 0177332-A 73 18-OCT-2001;
Heska Corporation (US)
Location/Qualifiers
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/db_xref="taxon:9615"
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Best Local Similarity 99.8%; Pred. No. 3.9e-182;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 12
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LOCUS AX280345 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 80 from Patent WO0177332.
ACCESSION AX280345
VERSION AX280345.1 GI:16607723
KEYWORDS
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ORGANISM dog.
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (sites)
Mccall,C.A. and Tang,L.
Compositions and methods related to canine igg and canine il-13
receptors
Patent: WO 0177332-A 80 18-OCT-2001;
Heska Corporation (US)
Location/Qualifiers
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BASE COUNT 512 a 388 c 379 g 407 t
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Query Match 65.2%; Score 947.8; DB 6; Length 1686;
Best Local Similarity 99.8%; Pred. No. 3.9e-182;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 13
AX280347/c
LOCUS AX280347 1686 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 82 from Patent WO0177332.
ACCESSION AX280347
VERSION AX280347.1 GI:16607725
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (sites)
AUTHORS McCall,C.A. and Tang,L.
TITLE Compositions and methods related to canine igg and canine il-13
JOURNAL Patent: WO 0177332-A 82 18-OCT-2001;
receptors
Heska Corporation (US)
FEATURES
source
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/organism="Canis familiaris"
/db_xref="taxon:9615"
BASE COUNT 407 a 379 c 388 g 512 t
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Query Match 65.2%; Score 947.8; DB 6; Length 1686;

Best Local Similarity 99.8%; Pred. No. 3.9e-182;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 14
AX280342
LOCUS AX280342 1692 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 77 from Patent WO0177332.
ACCESSION AX280342


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VERSION          AX280342.1  GI:16607720
KEYWORDS
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ORGANISM          dog.
                  Canis familiaris
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE
AUTHORS          Mccall,C.A. and Tang,L.
TITLE            Compositions and methods related to canine igg and canine il-13
                  receptors
JOURNAL          Patent: WO 0177332-A 77 18-OCR-2001;
                  Heska Corporation (US)
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Best Local Similarity 99.8%; Pred. No. 3.9e-182;
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:52:01 ; Search time 31.88 Seconds
(without alignments)
2094.606 Million cell updates/sec

Title: US-09-828-995B-61

Perfect score: 2132

Sequence: 1 MAFIHLDVGLYLLVCTAF.....LLKTIPTHKVEFSHQDTFC 386

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
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- 9: sp_phase:*
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- 11: sp_protent:*
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- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1271.5	59.6	383	11	O88786	O88786 mus musculus
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4	318.5	14.9	427	4	Q96BB4	Q96bb4 homo sapien
5	313	14.7	396	4	Q14631	Q14631 homo sapien
6	312	14.6	420	4	Q14633	Q14633 homo sapien
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8	298	14.0	333	4	Q15469	Q15469 homo sapien
9	297.5	14.0	415	11	Q920K4	Q920k4 cavia porce
10	286	13.4	349	6	O97597	O97597 bos taurus
11	283.5	13.3	414	11	Q920B8	Q920b8 rattus norv
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25	178.5	8.4	622	6	Q9N0J7	Q9n0j7 callithrix
26	177	8.3	346	13	Q93404	Q93404 oreochromis
27	177	8.3	538	13	Q9DFU0	Q9dfu0 sparus aua
28	176.5	8.3	217	6	O46386	O46386 mustela vis
29	175.5	8.2	611	13	Q9PTH9	Q9pth9 xenopus lae
30	172.5	8.1	288	4	Q96P36	Q96p36 homo sapien
31	172.5	8.1	349	4	Q9UHJ5	Q9uhj5 homo sapien
32	172.5	8.1	376	4	Q96P35	Q96p35 homo sapien
33	163	7.6	206	4	O16354	O16354 homo sapien
34	161.5	7.6	636	13	Q90Z16	Q90zi6 paralichthy
35	143.5	6.7	198	6	O18985	O18985 cervus elap
36	143	6.7	425	11	Q9JM58	Q9jms8 mus musculu
37	142	6.7	638	13	Q9DE08	Q9de08 oncorhynchu
38	142	6.7	918	13	Q9W609	Q9w6u9 gallus gall
39	140	6.6	422	4	O75462	O75462 homo sapien
40	140	6.6	422	4	Q9UHH5	Q9uhh5 homo sapien
41	139.5	6.5	881	13	O57519	O57519 xenopus lae
42	139	6.5	894	6	Q9MYL1	Q9myl1 macaca mula
43	139	6.5	925	6	Q9MYK9	Q9myk9 macaca mula
44	139	6.5	1163	6	Q9MYL2	Q9myl2 macaca mula
45	139	6.5	1194	6	Q9MYL0	Q9myl0 macaca mula

ALIGNMENTS

RESULT 1

Q95LF0 PRELIMINARY; PRT; 386 AA.
 ID Q95LF0;
 AC Q95LF0;
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
 DE INTERLEUKIN 13 RECEPTOR ALPHA CHAIN 2.
 GN IL13RA2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21287533; PubMed=11389954;
 RA Tang L.;
 RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and
 RT alpha2) cDNAs and detection of corresponding mRNAs in canine
 RT tissues.";
 RL Vet. Immunol. Immunopathol. 79:181-195 (2001).
 DR EMBL; AF314533; AAL14887.1; -;
 KW Receptor.
 SQ SEQUENCE 386 AA; 45110 MW; A16FDF2DD023ED95 CRC64;

Query Match 100.0%; Score 2132; DB 6; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1.1e-170;
 Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAFIHLDVGLYLLVCTAFGSMLSNAEIKVNPQDFEIVDPGVLGYSLSLQWQPPFLPDN 60
 DB 1 MAFIHLDVGLYLLVCTAFGSMLSNAEIKVNPQDFEIVDPGVLGYSLSLQWQPPFLPDN 60
 QY 61 FFECTEYELKYRNIDSENNKTIITKNLHYKDGFDLNGKTEAKINTLLPAQCTNGSEVRS 120
 DB 61 FFECTEYELKYRNIDSENNKTIITKNLHYKDGFDLNGKTEAKINTLLPAQCTNGSEVRS 120
 QY 121 SWAETTYTSPQGNRETKIQDMDCVYVNMQYLVCWSKPGMGVHFDNTNYQLFYWYEGLDHS 180

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Db 121 SWAETTYWTSPOGNETRIKIDMDCVYNNQYLVCSWKPGRGVHFDNYQLFYWYEGLDHS 180
QY 181 AECTDYIKVNGKMGCRFPYLESSDYKDFYICVNGSSESOPIRPSYFIFOLQNIWKPMPP 240
Db 181 AECTDYIKVNGKMGCRFPYLESSDYKDFYICVNGSSESOPIRPSYFIFOLQNIWKPMPP 240
QY 241 DYLSLTVKNSSEINLKNMMPKGPPIPAKCFIYEIEFTEDGTTWTTTVENEIQITRTSNES 300
Db 241 DYLSLTVKNSSEINLKNMMPKGPPIPAKCFIYEIEFTEDGTTWTTTVENEIQITRTSNES 300
QY 301 QKLCFLVRSKVNITYCSDGDIWSWSDEQCKWGDIMWETLVFFLIPAFVIFVLVITCLL 360
Db 301 QKLCFLVRSKVNITYCSDGDIWSWSDEQCKWGDIMWETLVFFLIPAFVIFVLVITCLL 360
QY 361 LYKORALLKTIPTHTKKEVFSHQDTFC 386
Db 361 LYKORALLKTIPTHTKKEVFSHQDTFC 386

RESULT 2
ID O88786 PRELIMINARY; PRT; 383 AA.
AC O88786;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE IL-13 RECEPTOR ALPHA 2 (INTERLEUKIN 13 RECEPTOR, ALPHA 2).
GN IL13RA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN: C3H/HEJ; TISSUE: THYMUS;
RX MEDLINE: 98391042; PubMed: 9725226;
RA Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,
RA Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner K.J., Wood C.R.,
RA Collins M.;
RT "The murine IL-13 receptor alpha 2: molecular cloning,
RT characterization, and comparison with murine IL-13 receptor alpha 1.";
RL J. Immunol. 161:2317-2324(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U65747; AAC33240.1; -.
DR EMBL; BC003723; AAH03723.1; -.
DR HSSP; P16471; 1BP3.
DR MGD; MGI:1277954; Il13ra2.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003532; Hematopo_receptor_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 383 AA; 44482 MW; C25212325C47E35B CRC64;

Query Match 59.6%; Score 1271.5; DB 11; Length 383;
Best Local Similarity 57.2%; Pred. No. 1.4e-98;
Matches 222; Conservative 71; Mismatches 88; Indels 7; Gaps 3;

QY 1 MAPHIDVGLYTLVCTAFGSMLSNAETKVNPPQDFEIVDPGYLGLSLQWQPPPLFPDN 60
Db 1 MAPVH--IRCLFILLCTITGYSL---EIKVNPQDFEILDPLGLLYLQWKPVPVIEK 55
QY 61 FKPCETIYELKYNIDSNWKTITIKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRS 120
Db 56 FKGCTLEYELKYNVDSDSWKTKITIRNLHYKDGFDLNGKIEGKIRTHLSEHCTNGSEVQS 115
QY 121 SWAETTYWTSPOGNETRIKIDMDCVYNNQYLVCSWKPGRGVHFDNYQLFYWYEGLDHS 180
Db 116 PWIEASTGISDEGSLETKIDMKCIYNNQYLVCSWKPGRKTVYSDNTYTMFFWYEGLDHA 175
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QY 181 AECTDYIKVNGKMGCRFPYLESSDYKDFYICVNGSSESOPIRPSYFIFOLQNIWKPMPP 240
Db 176 LQCADYLQHDKEKNVGCKLSNLDSSDYKDFYICVNGSKLEPIRSSYTFVQQLNIVKPLPP 235
QY 241 DYLSLTVKNSSEINLKNMMPKGPPIPAKCFIYEIEFTEDGTTWTTTVENEIQITRTSNES 300
Db 236 EPLHISVENSIDIRMKWSTPGGPIPPRCYTYEIVIREDDISWESATDKNDMKLKRANES 295
QY 301 QKLCFLVRSKVNITYCSDGDIWSWSDEQCKWGDIMWETLVFFLIPAFVIFVLVITCLL 360
Db 296 EDLCFFVRCKVNITYCADDGIWSESEECWEGYTGPDSKIIFIVPVCLEFFIFULLLCLI 355
QY 361 LYKORALLKTIPTHTKKEVFSHQDTFC 386
Db 356 VEKEEPEPTLSLHVDLNKEVCAYEDTLC 383

RESULT 3
ID Q90XP8 PRELIMINARY; PRT; 404 AA.
AC Q90XP8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INTERLEUKIN 13 RECEPTOR ALPHA-2.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID:8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Lockyer A.E., Jones C.S., Noble L.R., Verspoor E., Holland J.,
RA Secombes C.J.;
RT "Isolation and characterization of a putative interleukin 13 receptor
RT alpha-2 sequence from rainbow trout (Oncorhynchus mykiss).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF361437; AAL26927.1; -.
KW Receptor.
SQ SEQUENCE 404 AA; 46728 MW; 4B9B7E3F4CFFB6D6 CRC64;

Query Match 26.8%; Score 572; DB 13; Length 404;
Best Local Similarity 32.8%; Pred. No. 6.3e-40;
Matches 105; Conservative 69; Mismatches 142; Indels 4; Gaps 2;

QY 14 LLVCTAFGSMLSNAETKVNPPQDFEIVDPGYLGLSLQWQPPPLFPDNFKETIYELKYR 73
Db 13 LMLSDWSQCISKQSEFTVDPDENIGIDDPGLGLPLVTHWTAPASLTNLTACSMRYHLEYF 72
QY 74 NIDSENNKTIITIKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRSWAETTYWTSPOG 133
Db 73 NTYQSRWTVIRTVRTWYRAQFDLEKEVRVRISTLLGAGCTNGTELKSPETEMVLPNNITG 132
QY 134 NRETKIQDMDCVYNNQYLVCSWKPGRGVHFDNYQLFYWYEGLDHSAECTDYIKVNGKN 193
Db 133 PVSRSVQGGCCVYQKEFMECTWETGLEPTQSQYSLYFHWREMEQAECPQYIHSNGVR 192
QY 194 MGRFPYLESSDYKDFYICVNGSSESOPIRPSYFIFOLQNIWKPMPPDYLSLTVKNSSEI 253
Db 193 TGCKFTESLSESDENICINSSPEVLRSAPFSLQIQNVKPAATETVHLEASPDRL 252
QY 254 NLKNMMPKGPPIPAKCFIYEIEFTEDGT---TWTTTVENEIQITRTSNE-SQKLCFLVRS 309
Db 253 QVQMDLPNERIPRHLLEYEVEAREEGVGQPLQNRVNTMETUTLSMDGARRKCFVRVS 312
QY 310 KVNICYSDGDIWSWSDEQC 329
Db 313 RMHYCADRGFWSDWSHWC 332

RESULT 4
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Q96BB4 PRELIMINARY; PRT; 427 AA.
ID Q96BB4
AC Q96BB4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN 13 RECEPTOR, ALPHA 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015768; AAH15768.1; -.
KW Receptor.
SQ SEQUENCE 427 AA; 48676 MW; E6A42F7466A39A09 CRC64;

Query Match 14.9%; Score 318.5; DB 4; Length 427;
Best Local Similarity 25.5%; Pred No. 1.2e-18;
Matches 105; Conservative 64; Mismatches 176; Indels 67; Gaps 19;

QY 11 LYTLLVCTAFGSLN-AETKVNPPDPFEIVDPGYLGLYSLQWQPLFPDNFKECTIHEY 69
   : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 10 LWALLLCAGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTNPP--EGASSNCSLWY- 66

QY 70 LKYRNIDSENWKTITKNLHYKGFDLNKGIEAKINILL----PAQC-TNGSEVRRSSWAE 124
   : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 67 --FSHFGDKQDKLAP-----ETRRISIEVPLNERICLVQSGQCSSTNESEKPSILVE 115

QY 125 TTYWTSPOGNETRIQIDMDCVYNQWLVCSKGMGVHFDNTYQLFYWYEGLDHSAECT 184
   : ||| : | : : : | : : : | : ||| ||| ||| ||| : | : | : | : |
DB 116 KCI-SPEGDPESAVTELOCIWHNLSYMKCSWLFCGRNTSPDTNTLYLWHRSLEKIHOCE 174

QY 185 DYIKVGNKMGCRPPY--LESSDYKDPYICVNGSESOPIRPSYFIFQLQINIVKMPDPDY 242
   : : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : |
DB 175 NIFR-EGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSENIPLTSRKVPDPPHI 233

QY 243 LSLTVKNSSEINLKNWPKGPPIPAKCFIYEIEFTEDGTWTWTTVNEIQITRTSNESQK 302
   : : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : |
DB 234 KNLSEFHN-DDLYVQWENPQNF-I-SRCFLYEYEVNNS-----QTETHNVFYVQEAACENPE 286

QY 303 L-----CFLV-----RSKNIYC-SDDGIWSESDQCKGDIWKETLV 340
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 287 FERNVENTSEFWPGVLPDTLNTVIRVKTNKLCEYEDDKLWSNNSQEMSIICK---KRNST 343

QY 341 FFLIPAFVSIFVL-VITCLLLYKQRRALKTIFHTK-----KEYFSHOD 383
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 344 LYITMLLIIVPVIAGAIIVLLLYLKR--LKIIIFPIPDGKIKFEMFGDQN 393

RESULT 5
Q14631 PRELIMINARY; PRT; 396 AA.
ID Q14631
AC Q14631;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR TYPE 2 PRECURSOR.
GN HSIL5R2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RA MEDLINE=92121815; PubMed=1732409;
RX Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT "Molecular cloning and expression of the human interleukin 5

```

RT	receptor."
DR	J. Exp. Med. 175:341-351(1992).
DR	EMBL; X61177; CAA43484.1; "
DR	InterPro; IPR002996; CRLA.
DR	InterPro; IPR003532; Hematopo_receptor_SF2.
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW	Signal; Receptor.
FT	SIGNAL
FT	CHAIN
SQ	SEQUENCE 396 AA; 44998 MW; IAB60619842ACDA5 CRC64;
Query Match	14.7%; Score 313; DB 4; Length 396;
Best Local Similarity	28.9%; Pred. No. 3,1e-18;
Matches 103; Conservative	62; Mismatches 156; Indels 36; Gaps 15;
QY	23 MLSNAEIKVNPQDFEIVDPGYGLSYLSQWOPPLFPD-NFKECTIEYELKYRIDSSENWK 81
DB	22 LLPDEKISLLPPVNFITKVTG-LAOLVLLQWPN--PDQQRNVNLEYOVKINAPKEDDYE 78
QY	82 TIITKNLHYKDGFDLNLKGIEAKINTLLPAOCTNGSEVRSSAETTYTSPQGNRETKIQD 141
DB	79 TRITES---KCVTILHKGFSASVRTILO--NDHSLASSWASAEI-HAPGPSPTSIVN 131
QY	142 MDCVYNNQ-----YLVGSWKPGMGVHEDTNYQLFYWYEGLDHLSAECTDIYK-V 189
DB	132 LTCITNTEDNYSRLRSYQVSLHCTWLVTGTDAPEDTQFLYYRYG--SWTECOEYSKDT 189
QY	190 NGKNMGCRFP--YLESSDYKDFYICVNGSSSQIPRSPYFIFOLONIYKPMPPDYLSLTV 247
DB	190 LGRNIACWFPRTFILSKGRDMLAVLVNGSSKSHAIRPFDQLFALHAIDQINPP--LNVTA 247
QY	248 K-NSEETLNKNMKGPIPAKCFYIEIF--TEDQTTWTTTVENE-IQITRTSNESOKL 303
DB	248 EIEGTRLSIQEWKPVSAFPIHCFDEYVKIHNTRNGYLQIEKLMTNAFISII--DDLKY 304
QY	304 CFLVRKVNIVYCSDDGIWSESDSQCKGDTWKETLVFLFLFPFAPVSVFLVITCLL 360
DB	305 DVQVRAAVSSMCREAGLWSEWSQPIYVGNDEHKPLREWFVIVIMATICFILLISLI 361
RESULT	6
ID	Q14633 PRELIMINARY; PRT; 420 AA.
AC	Q14633;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	INTERLEUKIN-5 RECEPTOR. PRECURSOR.
GN	HSIL5R.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Carnivora; Insectivora; Hominoidea; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RN	SEQUENCE FROM N.A.
RP	TISSUE=PERIPHERAL BLOOD;
RC	MEDLINE=92121815; PubMed=1732409;
RA	Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT	"Molecular cloning and expression of the human interleukin 5
RT	receptor.";
RL	J. Exp. Med. 175:341-351(1992).
RL	EMBL; X61176; CAA43483.1; "
DR	InterPro; IPR002996; CRLA.
DR	InterPro; IPR003532; Hematopo_receptor_SF2.
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW	Signal; Receptor.
FT	SIGNAL
FT	CHAIN
SQ	SEQUENCE 420 AA; 47670 MW; 8DC56DFC8BEFF524 CRC64;
Query Match	14.6%; Score 312; DB 4; Length 420;

Best Local Similarity 28.6%; Pred. No. 4e-18;
Matches 102; Conservative 63; Mismatches 156; Indels 36; Gaps 15;

```
QY 23 MLSNAEIKVNPQDFEIVDPGVLGYLSLQWQPPDP-NFKECTIEYELKYRNIDSENWK 81
DB 22 LLPDEKISLPPVNFITKVYG-LAQVLLQWKPN--PDQQRNVNLEYQVKINAPKEDDYE 78
QY 82 TIITKNLHYKDGFDLNKIGAEAKINTLLPAQCTNGSVRSWAETTYWTSPQGNRETKIOD 141
DB 79 TRITES---KCVTILHKGSASVRTILQ---NDHSLASSWASAEI-HAPPGSPGTSIVN 131
QY 142 MDCVYVNWQ-----YLVCSWKPGMGVHFDNYQLFYWYEGLDHSAECTDYIK-V 189
DB 132 LTCTTNTTNDNYSRLRSYQVSLHCTVLGTDAPEDQYFLYRYG--SWTECQEQYSKDT 189
QY 190 NKGKMGCRPP--YLESSDYKDFYICVNGSSEOPRPSYFIFOLQNVKPMPPDYLSLTV 247
DB 190 LGRNACWFPFRFILSKGRDWLAVLVNGSKSHSAIRPFDFALHAIDQINPP--LNVT 247
QY 248 K-NSEINLKNWPKGPIPAKCFIYEIEF--TEDGTTWTTTVENE-IQITRTSNESQKL 303
DB 248 EIEGTRLSIQWEKPVSAFFIHCFDYEKIHNTNRNGYLQIEKLTNAFISII---DDLSKY 304
QY 304 CFLVRSKVNICYSDGINSWSEDEQWCKDIWKTILVFLIPFAFVSIFVLVITCLL 360
DB 305 DVQVRAAVSSMCREAGLWSEWSQPIYVGNDEHKPLREWFVIVIMATICFILLILSLI 361
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RESULT 7
Q95LF1 PRELIMINARY; PRT; 405 AA.
AC Q95LF1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE INTERLEUKIN 13 RECEPTOR ALPHA CHAIN 1 (FRAGMENT).
GN IL13RAL.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21287533; PubMed=11389954;
RA Tang L.;
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and
alpha2) cDNAs and detection of corresponding mRNAs in canine
tissues.";
RL Vet. Immunol. Immunopathol. 79:181-195(2001).
DR EMBL; AF314532; AAL14886.1; -.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 405 AA; 46328 MW; 926E1AC7BE5E3F42 CRC64;
```

Query Match 14.6%; Score 311; DB 6; Length 405;
Best Local Similarity 26.8%; Pred. No. 4.7e-18;
Matches 97; Conservative 59; Mismatches 156; Indels 50; Gaps 17;

```
QY 52 WQPLFPDPNFKECTIEYELKYRNIDSENWKTIITKNLHYKDGFDLNKIGAEAKINTLLPAQ 111
DB 30 WAPP--EGASPNCTLRY---FHFQDNKQDKIAPET-HRSKEYPLNERICLQVG----SQ 79
QY 112 C-TNGSEVRSSNAETTYTSPQGNRETKIODMDCVYVNWQYLVCSWKPGMGVHFDNYQL 170
DB 80 CSTNESDNPSILVEKC-TPPGEGDPSAVTELCQVWHNLSYMKCTWLPGRNTSPDNTYL 138
QY 171 FYWYEGLDHSAECTDYIKVNGKMGCRFPY--LESSDYKDFYICVNGSSEOPRPSYF 228
DB 139 YVWHSSLGKILQCEDIYR-EGQHIGCSFALTNLKDSFFQHSQVIMVKDNARKIRSFNI 197
QY 229 FOLQNTVKNMPDYLSLTVKNSEINLKNWPKGPIPAKCFIYEIEFTEDGTTWTTTVE 288
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DB 198 VPLTSHVKPDPPIHKRLFTQNG-NLYVQWKPNQ-FYSRCLSYQVEVNNSTQETNDFYV 255
QY 289 NEIQTRTNSQO---KLCFLV-----RSKNVIYC-SDDGIWSEHSDQCKW 331
DB 256 EBAKQNSFEQNEGLECTICFMVPGVLPDLTNTVRIKVRNKLCEYEDDKLWNNMQAM--- 312
QY 332 GDIMWETLVFFLIPFAFVSIFVL--VITCLLYKQALLKLTFTHTK-----KEVFESH 381
DB 313 -SIGENTDFTFYITMLLATQVIVAGAIILLLYLKR--LKIIFPPIPDGKIFKEMFGD 369
QY 382 QD 383
DB 370 QN 371
RESULT 8
Q15469 PRELIMINARY; PRT; 333 AA.
AC Q15469;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SOLUBLE INTERLEUKIN-5 RECEPTOR PRECURSOR.
GN HSIL5R4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=PERIPHERAL BLOOD; PubMed=1732409;
RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tominaga A., Takatsu K.;
RT "Molecular cloning and expression of the human interleukin 5
receptor.";
RL J. Exp. Med. 175:341-351(1992).
DR EMBL; X62156; CAA44081.1; -.
DR InterPro; IPR002996; CRIA.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW Signal; Receptor.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.
SQ SEQUENCE 333 AA; 37722 MW; 8D9239845E16985B CRC64;
```

Query Match 14.0%; Score 298; DB 4; Length 333;
Best Local Similarity 29.5%; Pred. No. 4.6e-17;
Matches 95; Conservative 57; Mismatches 134; Indels 36; Gaps 15;

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QY 23 MLSNAEIKVNPQDFEIVDPGVLGYLSLQWQPPDP-NFKECTIEYELKYRNIDSENWK 81
DB 22 LLPDEKISLPPVNFITKVYG-LAQVLLQWKPN--PDQQRNVNLEYQVKINAPKEDDYE 78
QY 82 TIITKNLHYKDGFDLNKIGAEAKINTLLPAQCTNGSVRSWAETTYWTSPQGNRETKIOD 141
DB 79 TRITES---KCVTILHKGSASVRTILQ---NDHSLASSWASAEI-HAPPGSPGTSIVN 131
QY 142 MDCVYVNWQ-----YLVCSWKPGMGVHFDNYQLFYWYEGLDHSAECTDYIK-V 189
DB 132 LTCTTNTTNDNYSRLRSYQVSLHCTVLGTDAPEDQYFLYRYG--SWTECQEQYSKDT 189
QY 190 NKGKMGCRPP--YLESSDYKDFYICVNGSSEOPRPSYFIFOLQNVKPMPPDYLSLTV 247
DB 190 LGRNACWFPFRFILSKGRDWLAVLVNGSKSHSAIRPFDFALHAIDQINPP--LNVT 247
QY 248 K-NSEINLKNWPKGPIPAKCFIYEIEF--TEDGTTWTTTVENE-IQITRTSNESQKL 303
DB 248 EIEGTRLSIQWEKPVSAFFIHCFDYEKIHNTNRNGYLQIEKLTNAFISII---DDLSKY 304
QY 304 CFLVRSKVNICYSDGINSWSEWS 325
DB 305 DVQVRAAVSSMCREAGLWSEWS 326
```

[illegible]

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RESULT      9
Q920K4      PRELIMINARY;          PRT;    415 AA.
ID Q920K4;
AC Q920K4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INTERLEUKIN-5 RECEPTOR ALPHA PRECURSOR.
GN GPIL-SRA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
NCBI_TaxID=10141;
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RT Norris T.E.;
RA "Cloning and Characterization of the Guinea Pig Interleukin-5 receptor
alpha cDNA.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U5215; AAD09361.1; -.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003532; Hematopo_receptor_S_F2.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
DR SIGNAL; Receptor.
FT CHAIN          18   415
FT CHAIN          18   415 INTERLEUKIN-5 RECEPTOR ALPHA.
SQ SEQUENCE       415 AA; 46913 MW; 41BA4BA597B31CD4 CRC64;

Query Match           14.0%; Score 297.5; DB 11; Length 415;
Best Local Similarity 27.2%; Pred. No. 6.5e-17;
Matches 107; Conservative 62; Mismatches 169; Indels 55; Gaps 18;

Qy 8 VGFLYTLVCTAFGSMLSNAEIKVNPPDOFPEIVDPGYLGYSLOWQPPLFPD-NFEKCTI 66
   :|: |: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: |
Db 9 LGAIETLTQDT-----LPDKRFLLPPIINFITKVGT-LAQVVLCWEPN--PNQGKNVL 60

Qy 67 EVELKYRIDSENKTIITKNLHKDGFDLNKGIEAKINTILLPAQTCSNGSEVRSSWAETT 126
   :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: |
Db 61 NYHWKIPNQEEHYE---TRNTQSKCETTLHQGVSAVRTIL---WHGSHLLASSWSVAE 114

Qy 127 YWTSPOQNRETKIQDDMCV-----YYNMQ----YLVCMSKPGMGVHFDNYQLFY--- 172
   :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: |
Db 115 H-KAPPSPGTSIVNLACTTTTAASNTYNLKSYESVSLHCTWLAKGDAPEDTQYFLYRYG 173

Qy 173 -WYGLDHSACTDYIK-VNCKNMGCRFP--YLESSDYKDFYICVNGSSESOPIRPSYFI 228
   ||: ||: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: |
Db 174 PWTE-----ECQEVSKDLSRNTACWPPTFIHISKARDRLAVHVNGSSNHATIKPFDL 227

Qy 229 FQLNIYKMPDPDYLSTLVKNSSEINLKWNPKGPISAKCFIYEIEP--TEDGTTWTITT 286
   ||: ||: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: |
Db 228 FDTQAIDQNPMPDMDTVAETEGS-RLSIQOWKPVSAFFIHCEFYEVKICTNDXYQVEKTT 286

Qy 287 VENEIQRTRNESOKLCLFLYRSKVNIVCSDDGIWSESDQCWKGDIIWKTLYEFFELIFP 346
   ||: ||: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: |
Db 287 TN---AFVSTTDGVSKSYIQVRAAVSPHCRRAMGLWSKWS-QPVVGKEKKKIAGWFILTL 342

Qy 347 AFVSIFVLVIITCLLYKQALLKTIHTTKKEVF 379
   | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: |
Db 343 TAVLCFILLIIFFLC-----RIYHLWTMKEF 367

RESULT      10
O97597
ID O97597      PRELIMINARY;          PRT;    349 AA.
AC O97597;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

```



```

Db      234 KNLSFHN-DDLYVQWENPQNFI-SRCLFYEVNNSQT 269
      :|: | :: ::| |: | ::| ||:|

```

RESULT

ID	QDEQ1	PRELIMINARY;	PRT;	343 AA.
AC	QDEQ1;			
DT	01-MAR-2001	(Tremblrel. 16, Created).		
DT	01-DEC-2001	(Tremblrel. 19, Last sequence update)		
DT	01-DEC-2001	(Tremblrel. 19, Last annotation update)		
DE	CYTOKINE RECEPTOR COMMON GAMMA CHAIN.			
OS	Oncorhynchus mykiss	(Rainbow trout) (Salmo gairdneri).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
ON	NCBI_Taxid=802;			
RX	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=21287902; PubMed=11394690;			
RA	Wang T., Secombes C.J.;			
RT	"Cloning and expression of a putative common cytokine receptor gamma			
RT	chain gene in rainbow trout (Oncorhynchus mykiss).";			
RL	Fish and Shellfish Immunol. 11:233-244 (2001).			
RL	EMBL; AJ276623; CAC09429.2;			
RT	Receptor.			
SK	SEQUENCE	343 AA; 39486 MW; ED8429EF7534B21EB CRC64;		

Query Match	10.7%	Score 228.5;	DB 13;	Length 343;
Best Local Similarity	25.3%	Pred. No. 3.2e-11;		
Matches	67;	Conservative 46;	Mismatches 105;	
		Indels 47;	Gaps 10;	

Qy	130	SPQGNRETKIQDMDCVYVNNQOYLVCSSWK-----PGMGVHEDTNTVOLPYWTEGLDHSACEDT	185
Db	13	SLOGYEAPSTPNVNCILINDYVNCIWSEQISIP-----EVNFTFFSSRFIDKNMEECTT	66
Qy	186	YIKVNGKMGRCRFPYLESSDYKDFYICVNGSSSQPIRPSYFTFQ---LQNIWKMPDPDY	242
Db	67	YLQESYAVGCRLSYDKSDRFR-----TLTKLVHQNMYSVQDHNLSKWKLYPPVN	118
Qy	243	LSLTVKNSSEINLKNWMPKGPIDPAKCFIYEIETEDGTWTVTTVYVNEIQ-IIRTSNESQ	301
Db	119	LSVMNNKDPELNLVYNNNSKNTF---CIESEVRVRIINSDKWKTSTPSKEQKAYAVAPLKSS	175
Qy	302	KLCFLVRSKSVNIYSCDDGINWSESDQCW---KGD-----IWKETLVFFELIPSA	347
Db	176	RYEQVQVRRVNDMCGESEFHWSEWSQPTQWDSMKGNITDSSGMSVWRPVL-----S	228
Qy	348	FVSIFVL-VITCLLLLYKORALLKTI	371
Db	229	LVGTMPTLFIACMLVYRERLRARI	253

RESULT 15

Q64146	Q64146	PRELIMINARY;	PRT;	896 AA.
ID	Q64146			
AC	Q64146;			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)		
DE	INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).			
GN	IL-3R<BETA>.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
EN	[1]			
RP	SEQUENCE FROM N. A.			
RA	MEDLINE=95370942; PubMed=7643220;			
RA	Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;			
RT	"Cloning of rat interleukin-3 receptor beta-subunit from cultured			
RT	microglia and its mRNA expression in vivo."			

RL J. Neurosci. 15:5800-5809(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-WISTAR; TISSUE=BRAIN;
RA Gebicke-Haerter P.J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ000555; CAA04186.1; -.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR00282; Cytok_receptor_2.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003531; Hematopoio_receptor_SF.

DR FIRM, F100041, IN3, 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE: PS01355: HEMATOPO REC S F1: UNKNOWN 1

Signal	1	1
FT NON_TER	896	896
FT NON_TER	896	896
SQ SEQUENCE	896 AA;	99504 MW;
		4C6E3B288A4A1052 CRC64;

Query Match	10.2%	Score 218.5	DB 11	Length 896
Best Local Similarity	22.0%	Pred. No. 7e-10		
Matches	81	Conservative	60	Mismatches 154
				Indels 73
				Gaps 16

QY 33 PPQDFEIVDPGYLSLWQPPLFPD--FKECTIEVELKYRNIDSENWKTIITKNLH 89
||| | | : ||| : ||| : : :
pb 138 PPKDISPSG--DHLELKWSVPLGDPAOVSLKODIOREAVAYKOL--OOSWD--ASSLH 192

QY 90 YKGFDLNKGIEAKINTLLP-----AQCTNGSEVR--SSWAETTYTSPQCNET 137
| : : | | | | : : : : : : : :
db 193 -----TCNLWVTLERKLELPNSIYVARVAOLAPGSSISGRPSGSPEVWDSPTEOK-A 246

QY 138 KIQMDCVVYNQWLYCSWKPGMGVHFDNTYQIFYWYEGLDHSACTDYIKVNGKNMGR 197
: l:: : : | | lll: | : : lll : : : : :
pb 247 RPONLCFFGIGIOSLNCSEWVNTKYTVDSVFGIFYSSSPKAGERKCSPPVK----- 297

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QY      198 FPYLESSDYKDFYICVNGSSSQPIRPSYFIFQLQNIWK-----PMPPDYLSLTV 247
      |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db      298 --EIOASRYTRYHCSLN---VSDPAAHSOYTVSVKRLGCKFIESFNHIOQNPPITLNT- 351

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QY	248	KNSEINLKNMMPKGP	IPAKCFIYEI	FTEDGTWTTT	VENEIQITRTS	NESQKL---	303
		:		: : : :	:	:	
Db	352	KNRQSYSLHWETOK	MSYPFIOHAF	OVYKKLDR	WEDSKTEN-----	LNHAHSMDLPO	404

QY 304 -----CFLRSKVNYCSDDGJWSEWDEQCWKGD-----IW-KETLVFFLIPFAFVSIF 352

Db 405 LEPGTSYCARVRKVTIPEYKGIWSEWSECTWTTDWMPTLWIVILVFLTLTFLALRF 464

Qy	353	VLVITCLL	360
		:	:
Db	465	GCIYGCKL	472

Search completed: September 20, 2002, 11:54:25
Job time: 144 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:51:31 ; Search time 21 Seconds
(without alignments)
1766.213 Million cell updates/sec

Title: US-09-828-995B-61
Perfect score: 2132
Sequence: 1 MAFIHLDVGLYTLVCTAF.....LLKTIPTKKEVFESHQDTFC 386
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	349.5	16.4	426	2 JC7773	IL-13ralpha 1 prot
2	312	14.6	420	2 S21052	interleukin-5 rece
3	298	14.0	335	2 A40267	interleukin-5 rece
4	266	12.5	415	2 S12357	interleukin-5 rece
5	256	12.0	831	2 J01655	prolactin receptor
6	232	10.9	369	2 A42565	interleukin-2 rece
7	221	10.4	878	1 A40091	interleukin-3 rece
8	221	10.4	896	1 A35782	cytokine receptor
9	218.5	10.2	896	2 I56563	interleukin-3 rece
10	217.5	10.2	830	2 I50455	prolactin receptor
11	216	10.1	373	2 A55718	interleukin-2 rece
12	208	9.8	369	2 I49280	interleukin-2 rece
13	195	9.1	581	2 I45971	prolactin receptor
14	194	9.1	310	2 A29884	prolactin receptor
15	194	9.1	412	2 A41070	prolactin receptor
16	194	9.1	610	2 A36116	prolactin receptor
17	193	9.1	610	2 A34631	lactogen receptor
18	192	9.0	897	1 A39255	cytokine receptor
19	189	8.9	292	2 I77525	prolactin receptor
20	189	8.9	303	2 I77524	prolactin receptor
21	189	8.9	608	2 I53269	prolactin receptor
22	180.5	8.5	630	2 I51086	prolactin receptor
23	178	8.3	616	2 A30304	prolactin receptor
24	172.5	8.1	288	2 B59405	prolactin receptor
25	172.5	8.1	376	2 A59405	prolactin receptor
26	172.5	8.1	622	2 A40144	prolactin receptor
27	154.5	7.2	917	2 I49699	glycoprotein 130 -
28	150	7.0	918	2 A36337	membrane glycoprot
29	145	6.8	918	2 A44257	interleukin-6 sign

30 144.5 6.8 400 2 S06945 granulocyte-macrop
31 143 6.7 333 2 S13684 granulocyte-macrop
32 143 6.7 378 2 S50040 granulocyte-macrop
33 136.5 6.4 638 2 S12136 somatotropin recep
34 131.5 6.2 378 2 A40266 interleukin-3 rece
35 130 6.1 150 2 B34631 lactogen receptor
36 127.5 6.0 638 2 B28176 somatotropin recep
37 127.5 6.0 800 1 S31575 interleukin-4 rece
38 127.5 6.0 1557 2 D41214 protein-tyrosine-p
39 127.5 6.0 1630 2 C41214 protein-tyrosine-p
40 127 6.0 286 2 S50039 granulocyte-macrop
41 124.5 5.8 1097 2 S17308 leukemia inhibitor
42 123.5 5.8 817 2 A48721 titin, muscle - ch
43 123 5.8 825 1 A60386 interleukin-4 rece
44 122.5 5.7 1825 2 C88400 protein H19M22.1 l
45 122.5 5.7 1825 2 T32828 hypothetical prote

ALIGNMENTS

RESULT 1
JC7773
IL-13Ralpha 1 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: JC7773
R:Pierrot, C.; Beniguel, L.; Beque, A.; Khalife, J.
Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A:Title: Expression of a functional IL-13Ralpha by rat B cells.
A:Reference number: JC7773; PMID:11573960
A:Accession: JC7773
A:Molecule type: mRNA
A:Residues: 1-426 <PIE>
A:Cross-references: CB:AY044251
C:Comment: This protein is an functionally binding protein involved in B cell prolife
C:Genetics:
A:Gene: il-13ralpha

Query Match	16.4%	Score 349.5;	DB 2;	Length 426;
Best Local Similarity	27.9%	Pred. No. 3.7e-19;		
Matches 113;	Conservative	65;	Mismatches 178;	Indels 49;
Gaps	18;			
Qy	10	FLYTLVCTAFGSLMSNAEI--KVNPPQDFEIVDPGYLGYSLSQWQPLFPDNEKECTIE	67	
Db	6	WLGELLVLLFAASLDQVALATEVOPVTNLSVSVENLCTIVTWTWSP--EGASPNCSLR	63	
Qy	68	YELKYRNIDSENWKTITTKNLHYKGFDLNKGIEAKINTLLPAQC-TNGSEVRRSSWAETT	126	
Db	64	Y---FSHFDDQDKKIAPETRRKE-LPLNE----KICLVGSGCSTNESEKPSPLVKKC	115	
Qy	127	YWTSPQGNRETKIQDMDCVYVNWQYLVCSWKPGMGVHFDTNQVLFYWFYEGLDHSAECTDY	186	
Db	116	I-SPRRGSESAVTELOCTWHNLSYMKCSWLPKGNWTSPTNTYLYWYSSLGKSLQC-EN	173	
Qy	187	IKVCKNMGCRFPYLE-SSDYKDFYICVNGSSSEOPRPSYFIFOLQIVKPMPPDYLSL	245	
Db	174	IHRGQHIGCSFKLTKEVSNYEHHNIQIMVKDNAGKIRPSKYIVTSNVRKPGPHIKHL	233	
Qy	246	TVKNSSEINLKNWMPKGPAPAKCFIYEIEFTDGT-TWTTTVEINEIQTITSNESQKL-	303	
Db	234	FLKNG-ALFVQWKPNQ-NFSSRCLSYEVEVNSTQDTSYNSNSLEVEEDKCNSEFDRNME	291	
Qy	304	---CFL-----VRSKVNIIYCSDDG-IWSEWSDQCWKGDITWKE-TLVFFFLIP	345	
Db	292	GASCFISPGVLXNTVYTVRVKTNKLCFDDNDLMSNNSEAL-----SIGKEPNSTFTTMM	347	
Qy	346	FAFYISFVLVITCLLYKQKRALTKTF-----HTKKEVFESHQD	383	
Db	348	LLIIPFVAVVAVIIILLFYLKRLKIIIFPPIDPDGKIFKEMFGDQN	392	

A:Cross-references: GB:D90205; NID:g220465; PIDN:BAAL4231.1; PID:g220466
C:Keywords: cytokine receptor; transmembrane protein

Query Match	12.5%	Score	266;	DB 2:	Length	415;			
Best Local Similarity	25.7%	Pred.	No. 8.6e-13;						
Matches	95;	Conservative	71;	Mismatches	166;	Indels	38;	Gaps	17;
Qy	8	VGFLYTLVCTAFGSMLSNAEIKVNPDPDFIVPGVGLYGLSLQWQPLFPD-NFKECTI	66						
Db	9	VGALATLQ-----ADLLNHHKFKLLPPVNFITIKATG-LAQVLLLHWDPN--PDQQRHVDL	60						
Qy	67	EYELKYRNIDSENWKTITITKNLHYKDGFDLANKGIEAKINTLLPAQCTNGSEVRSSWAETT	126						
Db	61	EYHKVINAPQDEYDTRKTES---KCVTPLHEGFAASVRTILKSHTT---LASSWVSAAE	114						
Qy	127	YWTSPQGNRETRKIODMDCVYN-----WQY-LVCSMKPGMVHFDNYQLFYWE	175						
Db	115	L-KAPSGPGSVTNLFTCTHTTVVSSVTHLRLPYQVSLKCTVLVGDKAPEDTQYLYLYRFG	173						
Qy	176	GLDHSACTDYIK-VNGKNMGCREP--VLESDDYKDFYICVNGSSESQIPRPSFYFIQLQ	232						
Db	174	VL--TEKCOEYSRDALNRNTACWFPRTFINSGFQEQLAVHINGSKSKAAIKPFDQLFSPL	231						
Qy	233	NIVKPMPPDYLILVKNSEENLNKNWPKGIPAKCFIYEIEF--TEDGTTWVTTTVEENE	290						
Db	232	AIDQVNPVRNVTVEIE-SNSLYIQWEKPLSAFFPDHCFNVELKIYNTKNGHIOKEKLIANK	290						
Qy	291	IQIPTRNESQKCLFLVRSKYNIYVCSDDGIWSESDQCKWGDILWKEFLVFLFIPFAEVS	350						
Db	291	F-ISKIDVVS-TYSIQVRAAVSSFCRMPGRNGEWS-QPIYVGKERKSLVHWHLIVLPAA	347						
Qy	351	IFVLIVITCLL	360						
Db	348	CFVLLIFSLI	357						

RESULT 5

JQ1655

prolactin receptor precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000

C:Accession: JQ1655

R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.

Biochem. Biophys. Res. Commun. 185, 490-496, 1992

A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence

A:Reference number: JQ1655; MUID:93075121

A:Accession: JQ1655

A:Molecule type: mRNA

A:Residues: 1-831 <TAN>

A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849

A:Experimental source: kidney

C:Superfamily: cytokine receptor homology

C:Keywords: glycoprotein; transmembrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-831/Product: prolactin receptor #status predicted <MAT>

F:36-219/Domain: cytokine receptor homology <CRS2>

F:239-425/Domain: cytokine receptor homology <CRS2>

F:439-462/Domain: transmembrane #status predicted <TM>

F:59-91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (covale

```

Query Match      12.0%; Score 256; DB 2: Length 831;
Best Local Similarity 25.4%; Pred. No. 1.2e-11;
Matches 100; Conservative 58; Mismatches 161; Indels 74; Gaps 19;

Qy 15 LVCTAFGSMLSNAEIKVNPDDFE---IVDPG-----YLGYSLQWQPPLEP 58
   : || : || : || : || : || : || : || : || : || : || : ||
Db 101 ITVTATNEIGSNS-----SDPOYVDVTSIVQGPSPVNLTKRSANIMYLWAKNSPPLLA 156

Qy 59 DNFECTIEYELKYRNDSENKKIITKNLHYKQGFDLNKIGAEKINTL-----LPAQ 111
   | |||| : || : || : || : || : || : || : || : || : || : ||
Db 157 DASNHNLYHYELRIKPEKEEWEIF-----SYGVQTQCKINRLNAGMRVYVGVGR 205

```

Qy	112	CTNGSEVRSSWAETTYWTSPQ-NREPKIDMDCVYYNWOYLVCSSWKPGMGVHFDNRNQL	170
Db	206	CTLDPGSEWSSSRHILIPSGSQPPKPTIIRCSPEKETFTCWMKPGLDGGHTNYTL	265
Qy	171	FYWYEGLDHSAECTDYIKVCKNMGCRFPYLESSDYKDFYICVNGSSE--SQPIRPSYFI	228
Db	266	LYSKEGEEQVVECPDY-RTAGPN-SCYFDKKHSTFWTYNITVRATNMGSGNSDDPHY--	321
Qy	229	FOLQNIYKPPMPDYSLSTVKNSEIN-----LKNMNP-----KGPIPAKCIEYIEEF-	275
Db	322	VDVTYIVQOPPP--VNVTLLELKRPIRKPVLVLTWSPPLADVRSGWLTL-----YELRLK	376
Qy	276	TEDGTTWTTTVNENIQTITS-NEOKLCLFVRSKVNIIYCSDD--GIWSEWSEDEQWK-	331
Db	377	PEEGEWEETIFVGQOTQYKMFSLPGKKYI-----IQIHCXPDHGSWSESENYYIQI	430
Qy	332	-GDIWKETLFFFLIPFAFVSIFVLVITCLLLYK	363
Db	431	PNDFRVDRMIVWVLGVLLSLCLIMSWTWLKL	463
RESULT	6		
	A42565	interleukin-2 receptor gamma chain - human	
	C:Species:	Homo sapiens (man)	
	C:Date:	04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000	
	C:Accession:	A42565; #accession_revision 154332	
	R:Takeshita, T.; Asao, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.;		
	Science	257, 379-382, 1992	
	A:Title:	Cloning of the gamma chain of the human IL-2 receptor.	
	A:Reference number:	A42565; MUID:92335883	
	A:Accession:	A42565	

A:Molecule type: nucleic acid; protein
A:Residues: 1-369 <TAK>
A:Cross-references: GB:D11086; NID:g303611; PIDN:BAAO1857.1; PID:g219890
A:Experimental source: MOLT beta lymphoid cells
A>Note: sequence extracted from NCBI backbone (NCBIP:l09167)
R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.
J. Biol. Chem. 268, 13601-13608, 1993
A>Title: Characterization of the human interleukin-2 receptor gamma chain
A:Reference number: A46591; MUID:G3293887
A:Accession: A46591
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058
R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Wilk
Hum. Mol. Genet. 2, 1099-1104, 1993
A>Title: The interleukin-2 receptor gamma chain maps to Xql3.1 and is muta
A:Reference number: I54332; MUID:94004847
A:Accession: I54332
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:I19546; NID:g349631; PIDN:AAC37524.1; PID:g349632
C:Genetics:
A:Gene: GDB:IL2RG; SCIDX1; IMD4
A:Cross-references: GDB:I34807; OMIM:308380
A:Map position: Xql3.1-Xql3.1
A:Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2; 308/3
A>Note: defects are associated with an X-linked form of severe combined im
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combi

Query Match 10.9% Score 232; DB 2; Length 369;
Best Local Similarity 24.1%; Pred. No. 2.9e-10;
Matches 65; Conservative 48; Mismatches 123; Indels 34; Gaps

Qy 125 TTYWTSPOGNRET-----KIQDMDCVYNNQYLVCNKPGMGVHFD 165
|| || || | : : : | : | : | : | : |
: : : | : | : | : | :

Db 25 TWTILT-PNGNEDTTADFFLTMTPTDLSVSTLPLPEVQCFVFNVEYMNCTWNSSEPO-P 82
QY 166 TNYQLFYWYEGDHS--ABCTDYIKVNGKNMGCRPPYLESSDYKDFYICVNGSSSQPTR 223
Db 83 TNLTLHYWYKNSDNQVKQSHYLFSEETISGQLOKKEIHLIYQTFVVLQDPRE--PRR 140
QY 224 PSYFIQQLQNIYKPPHPPDLSLTVKNSEINLKNWMPGPIPAKCFIVEIETED-GTTW 282
Db 141 QATQMLKQLNLVWAPENLTLKLSQLELNN--NRFLNHCLEHLVQVYRTDWDHSW 197
QY 283 VTTTVEIETQITRTSNESOK-LCFVLRKVNITYCSDGIGWSEWSDEQCKGDIWKETLVF 341
Db 198 TEQSDYDHRKFLSLPVDQGRYTFVRSRFNPLCGSAQWSEWSPHIHWSNTSKENPFL 257
QY 342 FLIPEAFVSI----FVLVITCLLYKQAL 367
Db 258 FALAVVTSVSGMGLIISLLCYVFWLERTM 287
RESULT 7
A40091
Interleukin-3 receptor beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A40091; A43022
R:Itoh, N.; Yonehara, S.; Schreurs, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara, I.
Science 247, 324-327, 1990
A:Title: Cloning of an interleukin-3 receptor gene: a member of a distinct receptor gene
A:Reference number: A40091; MUID:90117145
A:Accession: A40091
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-878 <I>
R:Gorman, D.M.
submitted to GenBank, November 1989
A:Reference number: A43022
A:Accession: A43022
A:Molecule type: mRNA
A:Residues: 1-815, 'Q', 817-878 <GOR>
A:CROSS-references: GB:M29885; NID:g198342; PIDN:AAA39295.1; PID:g309406
C:Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains
receptors.
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-878/Product: interleukin-3 receptor beta chain #status predicted <MAT>
F:23-440/Domain: extracellular #status predicted <EXT>
F:39-236/Domain: cytokine receptor homology <CRS1>
F:254-433/Domain: cytokine receptor homology <CRS2>
F:441-462/Domain: transmembrane #status predicted <TM>
F:463-878/Domain: intracellular #status predicted <INT>
Query Match 10.4%; Score 221; DB 1; Length 878;
Best Local Similarity 24.5%; Pred. NO. 6e-09;
Matches 86; Conservative 58; Mismatches 155; Indels 52; Gaps 19;
QY 33 PPQDFEIVDPGVLGSLQWQPLFPDN--FKECTIEYELKYNIDSENWKTITKNLH 89
Db 139 PKPDTHISPSG--DHFLLEWSVSLGDSQVSWLSSKDIEFEVAYKRL-QDSWED--ASSLH 193
QY 90 YKDGFDLNGKIBAKI---NTLLPA----QCTNGSEVR---SSWAETTYWTSPOGNETKI 139
Db 194 -TSNQVN--LEPKFLPNSIYAARVTRLSAGSSLSGRSPSWSEVHWDSQPGDK-AQP 249
QY 140 QMDCVYNNQWLVCSWPKGMGVHEDTNYQLFYWYEGDLSAECTDYIKVNGKNM----G 195
Db 250 QLLQCFDGIQSLHCSWEVWTTQTSVSGFLYRPSAPAEKSPVVKPEQASVYTRYR 309
QY 196 CRFPYLESSDYKDFYICVNGSSSQPTRPSYFIQQLQNIYKPPDLSLTVKNSEINL 255
Db 310 CSLPPEPSAHSQYTVSVKHLQGGKFIHSYHI-----QMEPPIILNQT-KNRDSYSL 360

QY 256 KWNMPKGPAPAKC-FIYEIEFTEDGTWTTTVEIETQITRTS-----NESQKLCFLVRSK 310
Db 361 HWETOK--IPKYIDHTFQVQYKKSKESWKSXTENLGRVNSMDLPQLEPDTSYCARVRVK 418
QY 311 -VNIYCSDDGIWSEWSDEQCKGDIWKETLVFLFPFAPVSVFVLVITCLL 360
Db 419 PTSDY---DGIWSEWSNEVWTTDWMPTLWILI-----LVFLIFTLLL 460
RESULT 8
A35782
cytokine receptor common beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A35782
R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Arai, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like pro
tein
A:Reference number: A35782; MUID:90319131
A:Accession: A35782
A:Molecule type: mRNA
A:Residues: 1-896 <GOR>
A:CROSS-references: GB:M34397; NID:g191821; PIDN:AAA37204.1; PID:g309101
C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 rece
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-896/Product: cytokine receptor common beta chain #status predicted <MAT>
F:23-441/Domain: extracellular #status predicted <EXT>
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-434/Domain: cytokine receptor homology <CRS2>
F:442-463/Domain: transmembrane #status predicted <TM>
F:464-896/Domain: intracellular #status predicted <INT>
Query Match 10.4%; Score 221; DB 1; Length 896;
Best Local Similarity 22.6%; Pred. NO. 6.1e-09;
Matches 90; Conservative 64; Mismatches 153; Indels 92; Gaps 21;
QY 31 VNPPQDFEIVDPGILGY-----LSLQWQPLFPDN----- 60
Db 100 VPIYTRFSTNEDYFSRPSDGLQLMVLAQNVQPLP-PKNVSISSSEDRFLEWSVS 158
QY 61 -----FKECTIEYELKYNIDSENWKTITKNLHYKDGFDLNGKIEAKI----- 104
Db 159 LGDAQVSWLSSKDIEFEVAYKRL-QDSWED--AYSILH-TSKFQVN--PEPKFLPNSIYA 212
QY 105 ----NTLLPAQCTNGSEVRSSWAETTYWTSPOGNETKIQDMDCVYNNQWLVCSWPKGM 160
Db 213 PRVTRLYPGSSLSGRP--SRWSPEAHWDSQPGDK-AQPQLQCFDGIQSLHCSWEVWT 269
QY 161 GVHFDNTYOLFVWYEGDLSAECTDYIK-VNGKNM-----GCRFPYLESSDYKDFYICVNG 215
Db 270 QTTGSVSGFLYRPSAPAEKSPVVKPEPPGASVTRYHCSLPLPEPSAHSQYTVSVK 329
QY 216 SSESQPIRPSYFIQQLQNIYKPPDLSLTVKNSEINLKNWMPGPIPAKCFI---YE 272
Db 330 LQGGK-----FIMSYNHI--QMEPTLNT-KNRDSYSLHWETOK---MAYSFIEHTTQ 377
QY 273 IEFTEDGTWTTTVEIETQITRTSNESQ---KLCFLVRKVNITYCSDGIGWSEWSDEQCK 329
Db 378 VOYKKKSDSWEDSKTEN-LDRAHSMDSLSQLEPDTSYCARVRVKPISNYDGIWSEVYT 436
QY 330 WKGD-----IKKETLVFLFPFAPVSVFVLVITCLLYK 363
Db 437 WKTDMVWMPFLWILVLI-----LTLILLIRFGCVSVYR 472
RESULT 9
I56563
Interleukin-3 receptor beta-subunit - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999

C:Accession: I56563
R:Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and
A:Reference number: I56563; MUID:95370942
A:Accession: I56563
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-896 <RES>
A:Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
C:Genetics:
A:Gene: rIL-3Rbeta
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor
F:39-235/Domain: cytokine receptor homology <CRS1>
F:253-433/Domain: cytokine receptor homology <CRS2>

Query Match 10.2%; Score 218.5; DB 2; Length 896;
Best Local Similarity 22.0%; Pred. No. 9.5e-09;
Matches 81; Conservative 60; Mismatches 154; Indels 73; Gaps 16;

Qy 33 PPODFEIVDVGVLGSLQWOPPLFPDN--FKECTIEYELKYRNIDSENKTIITKNLH 89
Db 138 PPKDISPSFG--DHFLKWSVPLGDAQVSLLSQKDIQFEVAYKOL-QDSWED--ASSLH 192

Qy 90 YKGFDFLNKGIEAKINTLLP-----AQCTNGSEYR---SSWAETTYWTSPQGNRET 137
Db 193 -----TCNLWLTLEPKLPNSIYVARVRAQLAPGSSLSGRPSGWSPEVHNDSPTEDK-A 246

Qy 138 KIQDMDCVYVNOYLVCWSKPGMGVHFDNTYOLFVWYEGLDHSAECTYIKVNGKMGCR 197
Db 247 RPQNLQCFDFGTSQSLNSWEVMTKVTDSVFGLEYSSSPKAGEKKCSPPWK----- 297

Qy 198 FPYLESSDYKDFYICVNGSSSESOPRPSYFFIFOLQNIYK-----PWPPDYLSLTV 247
Db 298 --ELQASRTYTHCSLN---VSDPAHSQYTVSVKRLQEQGFIESFNHIQNPPLNLT- 351

Qy 248 KNSSEINLKNWPKGPIPAKCFIYBIEFTEDGTTWTTTVEINEIQITRTSNESOKL----- 303
Db 352 KNRDYSYLHWETQKMSYFFIQAFOVQYKKLDRWEDSKTEN-----LNHSHMDLPQ 404

Qy 304 -----CFLVRSKVNIYSDGIGWSWSDEQCKWGD-----IW-KETLVFFLIPFAVSI 352
Db 405 LEPGTSYCARVRVKTIPYKGLWSEWSNECTWTTDWMPTLWLVILVFLTLFLALLRF 464

Qy 353 VLVITCLL 360
Db 465 GCIVGCKL 472

RESULT 10
150455
prolactin receptor - pigeon
C:Species: Columba livia (domestic pigeon)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
A:Accession: I50455
R:Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A:Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor.
A:Reference number: I50455; MUID:94283267
A:Accession: I50455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-830 <CH>
A:Cross-references: EMBL:U07694; NID:9466381; PIDN:AAA20646.1; PID:9466382
C:Superfamily: cytokine receptor homology
F:36-220/Domain: cytokine receptor homology <CRS1>
F:240-426/Domain: cytokine receptor homology <CRS2>

Query Match 10.2%; Score 217.5; DB 2; Length 830;
Best Local Similarity 25.7%; Pred. No. 1e-08;

Matches 87; Conservative 53; Mismatches 158; Indels 41; Gaps 16;

Qy 47 YLSLQWOPPLPDPNFKECTI-EYELKYRNIDSENKTIITKNLHYKDGFDLNKGIEAKIN 105
Db 145 YLLAKWSPPPLADVTSNSHVRYELRLKPEEKEWETV---SVGQVQYKYNR-LQAGVK 200

Qy 106 TLLPAQCTNGSEVRSSWAETTYWTSPOG-NRETKIQDMDCVYVNOYLVCWSKPGMGVHF 164
Db 201 YVQVRCVLDITGEMSEWSERHIHIPNGESPPEKPTIIFKRSPEKETTTCMWPKSGDGH 260

Qy 165 DTNYOLFVWYEGLDHSAECTYIKVNGKMGCRFPYLESSDYKDFYICVN-----GSSES 219
Db 261 PTNYTLLYSKGEERYECPDY-KTAGPN-SCYFDKKHTSFWTIYINIVKATNEIGSNVS 318

Qy 220 OPIRPSYFIFOLQNIYKMPDPDYLSL----TVKNSEELKNWMPKGPPIA-----KCFI 270
Db 319 DPL-----YVDVTYIVQTDPPVNVTLKKTIVNRKPVLVLTWSPD--PLADVRSGLTLD 371

Qy 271 YEIEF-TEDGTTWTTTVEINEIQITRTS-NESOKLCFLVRKVNIVYCSDD--GIWSEWSD 326
Db 372 YELRLKPEEAEWETIFVGQOQTHYKMFSLNPKKYI-----VQIHCKPDHHGSWSWSL 425

Qy 327 EQCKK--GDIWKETLVFFLIPFAVSIFFLVITCLLLYK 363
Db 426 EKYLOIPTDFRIKDMVWVWIIIVGVLSLLICLVMSWTWMLK 464

RESULT 11
A55718
interleukin-2 receptor gamma chain precursor - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 23-Jul-1999
A:Accession: A55718
R:Henthorn, P.S.; Somberg, R.L.; Elmiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg
Genomics 23, 69-74, 1994
A:Title: IL-2/gamma gene microdeletion demonstrates that canine X-linked severe combi
A:Reference number: A55718; MUID:95130114
A:Accession: A55718
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373 <H>
A:Cross-references: GB:U04361; NID:g517411; PIDN:AAC48403.1; PID:g517412
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication

Query Match 10.1%; Score 216; DB 2; Length 373;
Best Local Similarity 25.1%; Pred. No. 5e-09;

Matches 70; Conservative 51; Mismatches 128; Indels 30; Gaps 11;

Qy 104 INTLLPAQCTNGSE-----VRSSWAETTYWTSPQGNRETQIQDMDCVYVNOYLVCWS 156
Db 23 LNSTVP--MPGNEDITPDPFLTATPSETLSVSS-----LPLEVOQCFVFNVEYMNCTW 74

Qy 157 KPGMGVHFDNTYQFYWYEG--DHSACTYIKVNGKMGCRFPYLESSDYKDFYICVN 214
Db 75 NSSSEPR-PTNLT.LHWYKNSNDKQVQECGHYLSREVTAAGCWLQKEETHLYETEFVQLR 133

Qy 215 GSSESQPIRPSYFFIFOLQNIYKMPDPDYLSTLVKNSEELKNWMPKGPPIPAKCFIYEIE 274
Db 134 DPRE--PRRQSTQKLUKLQNLVPAPELTLHLNLSQLELSWS---NRHLDHCLHVVQ 188

Qy 275 FTED-GTTWTTTVEINEIQITRTSNESOKL-CFLVRKVNIVYCSDDGIWSEWSDQCKWG 332
Db 189 YRSDWDRSWTEQSDVDRHNSFSLPSVDGQKQFTYFRVRSRYNPLCCGSAQRWSEWSHPHIGS 248

Qy 333 DIWKETLVF----FLIPFAVSIFFLVITCLLLYKQRAL 367
Db 249 NTSKENPLFASEAVLPLGSLGLIISLI-CVYVWLERSI 286

RESULT 12
149280

interleukin-2 receptor gamma chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 20-Jun-2000
C:Accession: I49280; A47514; JN0592; JN0775; S37582; I53398
R:Cao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R) gamma chain
A:Reference number: A47514; MUID:93391374
A:Accession: I49280
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <CAO>
A:Cross-references: EMBL:U01795; NID:g727349; PIDN:AAA64279.1; PID:g727350
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-369 <RE2>
A:Cross-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068
R:Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K.
Biochem. Biophys. Res. Commun. 193, 356-363, 1993
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of function
A:Reference number: JN0592; MUID:93277575
A:Accession: JN0592
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <KUN>
A:Cross-references: DBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.
A:Reference number: JN0775; MUID:93366191
A:Accession: JN0775
A:Molecule type: mRNA
A:Residues: 1-369 <KOB>
A:Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1; PID:g436046
R:Chiu, R.K.; Dougherty, G.J.
submitted to the EMBL Data Library, October 1993
A:Description: Regulation of CD4-mediated cellular adhesion by the IL-2 R gamma chain.
A:Reference number: S37582
A:Accession: S37582
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>
A:Cross-references: EMBL:X75337
R:DiSanto, J.P.; Certain, S.; Willson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Sa
Eur. J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosomal location
A:Reference number: I53398; MUID:95104285
A:Accession: I53398
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-369 <RES>
A:Cross-references: GB:S75852; NID:g861554; PIDN:AAB32904.1; PID:g861555
C:Genetics:
A:Gene: IL-2Rgamma
A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3
C:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), beta (see PIR:UHMS2), and gamma (see PIR:UHMS2) subunits.
C:Function:
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK cells
C:Superfamily: interleukin-2 receptor gamma chain
C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-369/product: interleukin-2 receptor gamma chain #status predicted <MAT>
F:256-284/Domain: transmembrane #status predicted <TM>
F:171,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

QY 118 VRSSWAETTYTWTSPGONRETK-----IODMDCVYVYNWOYLVCWSKP 158
Db 19 LRAGSSKVLMS--ANEDIKADLILITSTAPHLASPTLPPEVOCFVFNIMYMNCTWS 76
QY 159 GMGVHFDTNVQLFYWYEGLDHSA--ECTDYIKVGNKMGCRFPYLESSDYKDFYICVNGS 216
Db 77 SSEPQ-ATNLTHRYRYKVSNNNTFQCSHYLSKETTSQCQIKEDIQLYQTFVVL--Q 133
QY 217 SESQPIRPSYFIFQQLQNVKMPDPYLSITVKNSEINLKNMKGPIPAKCFIYEIETP 276
Db 134 DPQKQRRRAVQKLNQNLVPRAPENLTLNLSUSESOLELRWK--SRHIKERCLQLVQYR 191
QY 277 ED-GTTTWTVTTEIQTIRTS-NEQKLCFLVRKVNICYSDDGISWSESDQCWKGDI 334
Db 192 SNDRSRTWELIVNHEPRFSLPSVDELKRYTFVRSYRNPICGSSQOWSKWSQPVHWSHT 251
QY 335 WKETLVFF-----LIPFAPVSIFVLVITCLLLY 362
Db 252 VEENPSLFALEAVLP--VGTMLIITLIFVY 281
RESULT 13
I45971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin receptor mRNA
A:Reference number: I45971; MUID:93246019
A:Accession: I45971
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C:Genetics:
A:Gene: PRLR
C:Superfamily: cytokine receptor homology
F:36-221/Domain: cytokine receptor homology <CRS>
Query Match 9.1%; Score 195; DB 2; Length 581;
Best Local Similarity 29.6%; Pred. No. 3.5e-07;
Matches 71; Conservative 31; Mismatches 88; Indels 50; Gaps 14;
QY 154 CSWKFGMGVHFDTNVQLFYWYEGLDHSAECTDYIKVGNKMGCRFPYLESSDYKDFYICV 213
Db 46 CWMEPCADGGTPTNVTLYHKEGTLIHCEPDY-KTGGPN-SCYFSKKHTSIWKMYVIT 103
QY 214 N-----GSSESQPIRPSYFIFQQLQNVKMPDPYLSITVKNSE-----INLKNMMP-KGP 263
Db 104 NAINOMGISSDPL-----YVHVTVIVEPPANITLLEKHPEDRKPYLWIKWSPTMTD 158
QY 264 IPAKCFI--YEIEF-TEDGTTWVT--TTVENEIQTIRTSNESQKLCFLVRKVNICYSD 318
Db 159 VKSGWFIQYIEIRLPERKATDNEHTFLKQTLKIFNL-YPQKYLVLQIRCK-----PDH 212
QY 319 GIWSEWSDQCKW-----GDIWKEPLVFFLIPFAPVSIFVL-----VITCLL 360
Db 213 GYWSEWSPESIQIPNDFPVKDTSMW----IFVAILSAVICLIIMVAVALKGYSMTCL 268
RESULT 14
A29884
prolactin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C:Accession: A29884
R:Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banvi
Cell 53, 69-77, 1988
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth
A:Reference number: A29884; MUID:88165059

Search completed: September 20, 2002, 11:53:46
Job time: 135 sec

QY 130 SPQGNRETKIQDMDCVYYNQYLVCSSKPGMGVHEDTNQLFYWYEGLDHSAECTDIKV 189
||| | : ||| | : ||| | : ||| |
Dd 21 SPGPKPEIH----KCRSPDKETFTCWNPPTDGGGLPNYSLTYSKEGETTYECDDY-KT 75

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OM protein - protein search, using sw model

Run on: September 20, 2002, 11:51:06 ; Search time 31.89 Seconds
(without alignments)
1344.449 Million cell updates/sec

Title: US-09-828-995B-61

Perfect score: 2132

Sequence: 1 MAFIHLVDVGLYLLVCTAF.....LLKTIPHTKKEVSHQDTFC 386

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

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19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2132	100.0	386	22 AAU69135	Canine interleukin
2	2021	94.8	365	22 AAU69136	Canine interleukin
3	1775	83.3	318	22 AAU69137	Canine IL-13R extr
4	1775	83.3	561	22 AAU69138	Canine IL-13Ralpha
5	1775	83.3	561	22 AAU69141	Canine IL-13Ralpha
6	1775	83.3	563	22 AAU69140	Canine IL-13Ralpha
7	1775	83.3	565	22 AAU69139	Canine IL-13Ralpha
8	1503	70.5	380	18 AAU24972	Human interleukin-
9	1503	70.5	380	18 AAU35295	Human IL-13 bindin
10	1503	70.5	380	18 AAU36613	Human Zcytor2 cyto
11	1503	70.5	380	19 AAU41520	Human Zcytor2 cyto

12	1503	70.5	380	19 AAU41502	Human cytokine/pep
13	1503	70.5	380	19 AAU33603	Homo sapiens HR-1
14	1503	70.5	380	21 AAU95296	IL-13 binding chai
15	1503	70.5	380	22 AAG63812	Amino acid sequenc
16	1503	70.5	380	22 AAG72136	Human interleukin
17	1503	70.5	380	22 AAB29748	Human IL-13 recept
18	1480	69.4	380	18 AAU36614	Human Zcytor2 cyto
19	1473	69.1	372	18 AAU36616	Celebub macaque Zc
20	1417	66.5	255	22 AAU69134	Canine interleukin
21	1392.5	65.3	315	19 AAU56261	Mature interleukin
22	1392.5	65.3	359	19 AAU56260	Construct containi
23	1271.5	59.6	383	18 AAU35294	Murine IL-13 bindi
24	1271.5	59.6	383	21 AAU95295	IL-13 binding chai
25	1271.5	59.6	383	22 AAU72135	Murine interleukin
26	1271.5	59.6	383	22 AAB29747	Mouse IL-13 recept
27	791	37.1	145	22 AAU69133	Canine interleukin
28	345	16.2	426	18 AAU09821	Mouse interleukin-
29	329	15.4	426	18 AAU09822	Human interleukin-
30	320	15.0	157	19 AAU56252	Interleukin-13 bin
31	318.5	14.9	427	18 AAU24973	Human interleukin-
32	318.5	14.9	427	22 AAB19807	Human interleukin-
33	316.5	14.8	427	22 AAB19808	Human interleukin-
34	314	14.7	396	13 AAR22216	Sequence of human
35	313	14.7	421	13 AAR25064	Human IL-5 recepto
36	312.5	14.7	396	13 AAR22220	Sequence of secret
37	312.5	14.7	420	13 AAR22219	Sequence of secret
38	312	14.6	420	19 AAU82842	Human interleukin-
39	311	14.6	405	22 AAU69132	Canine interleukin
40	306	14.4	420	13 AAR22215	Sequence of human
41	304.5	14.3	793	21 AAU92208	IL-13/IL-4 dual tr
42	301	14.1	313	18 AAU21856	Protein used in pr
43	298	14.0	335	13 AAR25063	Soluble human IL-5
44	298	14.0	335	14 AAR33699	shIL-5R-alpha. Sy
45	298	14.0	1026	16 AAR70121	IL5-R-GBP 130 fusi

ALIGNMENTS

```

RESULT 1
AAU69135
ID AAU69135 standard; Protein; 386 AA.
XX
AC AAU69135;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine interleukin 13 receptor PcaIL-13Ralpha2 386.
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI: 2001-657172/75.
DR N-PSDB; AA559562.
XX
PT Novel isolated canine protein, preferably canine immunoglobulin G

```

protein or canine interleukin-13 receptor protein useful for regulating
immune response of an animal and for developing regulatory compounds -
XX
PS Claim 20; Page 176-177; 221pp; English.

The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies raised against them, fusion proteins between the IgG and IL-13R proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence represents a protein of the invention.

SQ Sequence 386 AA;

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Query Match      100.0%; Score 2132; DB 22; Length 386;
Best Local Similarity 100.0%; Pred. No. 3e-198;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	1	mafthldvgflytlvctafgsmilsnaeikvnpqdpfeivdpgylylslqwpplfpdn	60
Qy	61	PKECTIEYELKYNIDSENKKTITTKNLHYKDGFDLANKIEAKINTLLPAOCTNGSEVRS	120
Db	61	fkectieyelkynidseknkttitknlhykdgfdlnkieakintllpactngsevrs	120
Qy	121	SWAETTYWTSPQGNRETKIOMDCVYVNWQYLVCSSWKPGMVHFDNTYNQLFYWYEGLDHS	180
Db	121	swaettywtspqgnretkiqdmcdvynwqylvcswkpgmvhfdntynqlfywyegldhs	180
Qy	181	AECTDYIKVNGKNMGRFPYLESSDYKDFYICVNGSSSQBPIRPSYTFIQNTIVKMPPP	240
Db	181	aectdyikvngknmgr-fpylessdykdfyicvngsssqbpirpsytfiqnkvkmppp	240
Qy	241	DYLSLTWKNSSEINLKNMPPKPTPAKCFYIEIEFTEDGTTWVTITVNETQIRTSNES	300
Db	241	dylsltwknsseinlknmpkpp-pakcfyieieftedgttwvtittvneteqirttsnes	300
Qy	301	QKICFLVRKVNICYSDGIGTWSHSDQCKGDIWKETLVFLFLPFPFVSFVLVITCLL	360
Db	301	qkicflvrskvnicysdgigtwsesdqckgdiwketlvflflpfpfvsfvlvitcll	360
Qy	361	LYQORALLKTIFFHTKKEVFSHQDTFC	386
Db	361	lyqorallktiffhtkkevfsdqdtfc	386

RESULT	2	
AAU69136		
ID	AAU69136 standard; Protein; 365 AA.	
XX		
XX	AAU69136;	
DT		
DT	29-JAN-2002 (first entry)	
XX		
XX	Canine interleukin 13 receptor PcaIL-13Ralpha2 365.	
DE		
XX		
KW	Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;	
KW	IL-13Ralpha1; IR-13Ralpha2; immunoglobulin heavy chain; IgG FC;	
KW	immunoglobulin light chain; lambda; immunosuppressive; gene therapy;	
KW	immune response.	
XX		
OS	Canis familiaris.	
XX		
PN	WO200177332-A2.	

XX	18-OCT-2001.	
PD		
XX		
XX	09-APR-2001; 2001WO-US11498.	
PF		
XX		
XX	07-APR-2000; 2000US-195659P.	
PR		
PR	07-APR-2000; 2000US-195874P.	
XX		
XX	(HESK-) HESKA CORP.	
PA		
XX		
XX	McCall CA, Tang L;	
PI		
XX		
DR	WPI; 2001-657172/75.	
DR	N-PSDB; AAS99966.	
XX		
PT	Novel isolated canine protein, preferably canine immunoglobulin G	
PT	protein or canine interleukin-13 receptor protein useful for regulating	
PT	immune response of an animal and for developing regulatory compounds -	
XX		
PS	Claim 20; Page 181-183; 221pp; English.	
XX		
CC	The invention concerns an isolated canine protein, preferably canine	
CC	immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)	
CC	receptor protein, the nucleic acids encoding them, antibodies	
CC	raised against them, fusion proteins between the IgG and IL-13R proteins	
CC	and methods of isolating regulators of them. The regulators are useful	
CC	for regulating an immune response in a canine. The proteins are useful	
CC	to develop regulatory compounds including inhibitors and activators that,	
CC	when administered to a canine in an effective manner, are capable of	
CC	protecting canine from disease mediated by IL-13Ra1pha or IL-13. The	
CC	regulators are useful for treating canine IgG (heavy and/or light chain)	
CC	and/or canine IL-13R mediated responses. The molecules of the invention	
CC	are useful to regulate the immune response of an animal (e.g. by gene	
CC	therapy). The present sequence represents a protein of the invention.	
XX		
SQ	Sequence 365 AA;	

Query Match	94.8%;	Score 2021;	DB 22;	Length 365;
Best Local Similarity	100.0%;	Pred. No. 1.6e-187;		
Matches 365;	Conservative 0;	Mismatches 0;	Indels 0;	Caps 0;
Qy	22	SMLSNAEIKVNPDPDFIVDPGYLGYSLOWQPPDPDNFEKCTIEYELKYRNIDSENWK	81	
Db	1	smlsnaeikvnpdpdfeivdpgylgylslwqppldfnfkectieyelkyrnidsenwk	60	
Qy	82	TIITKNLHYKDGFDLNGKIGIEAKINTLLPAOCTNGSEVRSSWAETTYWTSPOGNRETQID	141	
Db	61	tiiitknlhykdgfdlنگkieakintllpaqctngsevrsswaettywtspqgnretkigd	120	
Qy	142	MDCVYVNNQVILVCSWKGPMGVHDPTNYQLFWYEGLDHSAECTDYIKVNGCKNMCCRPPYL	201	
Db	121	mdcvyywnqylvcswkgpvmgvhfdtnyqlfwyegldhsaectdyikvنگkngmcrfpyl	180	
Qy	202	ESSDYKDFYICVNGSSSQPIRPSYFIFQLONIVKPMPPDYLSLTVKNSEINLKNMMPK	261	
Db	181	essdykdfyicvngsssqpirpsyfifqilnivkvpmpdyilsitvknseinlknmmpk	240	
Qy	262	GPAPAKCFIYEIETEDGTTWTTVNEIQTIRTSNESOKLCLFLVRSKNYICSDDGIIW	321	
Db	241	gpapakcfiyeletdgttwttvneiqirtsnesqklcflvrsknyicsddgilw	300	
Qy	322	SEWSDEOCWKGDIMKWTFLVFLPIPPAFVSVFLVITCLLYKQRALIKTIFHTKKVEFSH	381	
Db	301	sewsdeocwkgdikwrtlvflfplpafvsvflvitcllykqrallktifhtkkvefsh	360	
Qy	382	QDTFC	386	
Db	361	qdtfc	365	

RESULT 3
AAU69137

ID AAU69137 standard; Protein: 318 AA.
AC AAU69137;
XX
XX
XX 29-JAN-2002 (first entry)
XX
XX Canine IL-13R extracellular domain PcaIL-13Ralpha2 318.
XX
XX Dog; interleukin-13 receptor alpha; interleukin-13 receptor alpha2;
KW IL-13Ralpha; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
KW immune response.
XX
XX Canis familiaris.
XX
XX OS
XX PN WO200177332-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 09-APR-2001; 2001WO-US11498.
XX
XX PR 07-APR-2000; 2000US-195659P.
XX PR 07-APR-2000; 2000US-195874P.
XX
XX PA (HESK-) HESKA CORP.
XX
XX PT McCall CA, Tang L;
XX
XX DR WPI: 2001-657172/75.
XX DR N-PSDB; AAS59968.
XX
XX PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX PS Claim 20; Page 185-187; 21pp; English.
XX
XX CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence represents a protein of the invention.
XX
XX SQ Sequence 318 AA;

Query Match 83.3%; Score 1775; DB 22; Length 318;
Best Local Similarity 100.0%; Pred. No. 1e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 82 TIITKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVSSWAETTYMTSPGNNRRTKIQD 141
Db 62 tiitknlhykgdgdflnkgieakintllpaqctngsevrsswaettywctspgngnrtrtkiqd 121

Qy 142 MCVYVYNNQYLVCSMKPGMGVHFDNTNQLFYWYEGSLDHSACTDYIKYNGKNMGCRFPYL 201
Db 122 mdcvynvnyqylvcsmkpgmgvghfdntnqlfywyegldhsaectdyikvngknmgcrfpyl 181

Qy 202 ESSDYKDFYICVNGSSSQIRPSYFIIFQLQNIYKMPDPDYLSLTIVKNSSEINLKNWMPK 261
Db 182 essdykdfyicvngsssqirpsyfiifqlqnlvkmppdyllsltkvknseeinlknwmpk 241

Qy 262 GPIPAKCFIYEIEFTEDGTTWVTTTENEIQITRTSNESQKLCFLVRSKVNIYCSDDGIW 321
Db 242 gpipakcfiyeieftedgttwvtttteneiqitrtsnesqklcflvrskvniycsddgiw 301

Qy 322 SEWSDEQCWKGDWKET 338
Db 302 sewsdeqcwkgdwket 318

RESULT 4
AAU69138
ID AAU69138 standard; Protein: 561 AA.
XX
XX AC AAU69138;
XX
XX DT 29-JAN-2002 (first entry)
XX
XX DE Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-3523 561.
XX
XX KW Dog; interleukin-13 receptor alpha; interleukin-13 receptor alpha2;
KW IL-13Ralpha; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
KW immune response.
XX
XX CC Canis familiaris.
XX
XX OS
XX PN WO200177332-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 09-APR-2001; 2001WO-US11498.
XX
XX PR 07-APR-2000; 2000US-195659P.
XX PR 07-APR-2000; 2000US-195874P.
XX
XX PA (HESK-) HESKA CORP.
XX
XX PT McCall CA, Tang L;
XX
XX DR WPI: 2001-657172/75.
XX DR N-PSDB; AAS59970.
XX
XX PT Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
XX PS Claim 46; Page 191-193; 221pp; English.
XX
XX CC The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene
CC therapy). The present sequence represents a protein of the invention.
XX
XX SQ Sequence 561 AA;

Query Match 83.3%; Score 1775; DB 22; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.3e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 82 TITKLNHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRSSWAETTYWTSPQGNRETQIOD 141
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Db 62 ttiitknlhykdgfdlnkgleakintllpaqctngsevrsswaettywtspqgnrekiqd 121

QY 142 MDCVYNNWQYLVCSWKPGMGVHFDNTYQIFYWYEGLDHSAECTDYIKVNGKNMGCRFPYL 201
|||||
Db 122 mdcvyywnwqylvcswkpgmgvghfdntnyqifywyegldhsaectdyikvngknmgcrfpyl 181

QY 202 ESSDYKDFYICVNGSSESQPIRPSYFIFOLQNTVKKMPDPDYLSTLVKNSSEINLKNMMPK 261
|||||
Db 182 essdykdfyicvngssesqpirpsyfiglqnivkmpdpdyisltvknseeinlknwmpk 241

QY 262 GPIPAKCFIYEIEFTEDGTTWTTTVEINEIQITRTSNESQKLCFLVRSKVNIYCSDDGIW 321
|||||
Db 242 gpipakcfiyeieftedgttwtvtvneiqitrtstnesqklcflvrskvniycsddgiw 301

QY 322 SEWSDQCKWGDWIKET 338
|||||
Db 302 sewsdeqckwgdwiket 318

RESULT 5
AAU69141
ID AAU69141 standard; Protein; 561 AA.
AC AAU69141;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-B9 561.
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.
DR N-PSDB; AAS59976.
XX
PS Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS Claim 46; Page 210-212; 221pp; English.
XX
XX The invention concerns an isolated canine protein, preferably canine
CC immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13)
CC receptor protein, the nucleic acids encoding them, antibodies
CC raised against them, fusion proteins between the IgG and IL-13R proteins
CC and methods of isolating regulators of them. The regulators are useful
CC for regulating an immune response in a canine. The proteins useful to
CC develop regulatory compounds including inhibitors and activators that,
CC when administered to a canine in an effective manner, are capable of
CC protecting canine from disease mediated by IL-13Ralpha or IL-13. The
CC regulators are useful for treating canine IgG (heavy and/or light chain)
CC and/or canine IL-13R mediated responses. The molecules of the invention
CC are useful to regulate the immune response of an animal (e.g. by gene

CC therapy). The present sequence represents a protein of the invention.
XX
SQ Sequence 561 AA;

Query Match 83.3%; Score 1775; DB 22; Length 561;
Best Local Similarity 100.0%; Pred. No. 2.3e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 2 smlsnaeikvnpqgdfelvdpvgylglsiqwpplifpdnfkectieyleikyrnidsewk 61

QY 82 TITKLNHYKDGFDLNGKIEAKINTLLPAQCTNGSEVRSSWAETTYWTSPQGNRETQIOD 141
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QY 142 MDCVYNNWQYLVCSWKPGMGVHFDNTYQIFYWYEGLDHSAECTDYIKVNGKNMGCRFPYL 201
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QY 262 GPIPAKCFIYEIEFTEDGTTWTTTVEINEIQITRTSNESQKLCFLVRSKVNIYCSDDGIW 321
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Db 242 gpipakcfiyeieftedgttwtvtvneiqitrtstnesqklcflvrskvniycsddgiw 301

QY 322 SEWSDQCKWGDWIKET 338
|||||
Db 302 sewsdeqckwgdwiket 318

RESULT 6
AAU69140
ID AAU69140 standard; Protein; 563 AA.
XX
AC AAU69140;
XX
DT 29-JAN-2002 (first entry)
XX
DE Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-B9 563.
XX
KW Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2;
KW IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG Fc;
KW immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
KW immune response.
XX
OS Canis familiaris.
XX
PN WO200177332-A2.
XX
PD 18-OCT-2001.
XX
PF 09-APR-2001; 2001WO-US11498.
XX
PR 07-APR-2000; 2000US-195659P.
PR 07-APR-2000; 2000US-195874P.
XX
PA (HESK-) HESKA CORP.
XX
PI McCall CA, Tang L;
XX
DR WPI; 2001-657172/75.
DR N-PSDB; AAS59974.
XX
PS Novel isolated canine protein, preferably canine immunoglobulin G
PT protein or canine interleukin-13 receptor protein useful for regulating
PT immune response of an animal and for developing regulatory compounds -
XX
PS Claim 46; Page 203-206; 221pp; English.
XX


```
XX PD 12-JUN-1997.
XX XX
XX PF 07-NOV-1996; 96WO-FR01756.
XX XX
XX PR 06-DEC-1995; 95FR-0014424.
XX XX
XX PA (SNFI ) SANOFI SA.
XX PI Caput D, Ferrara P, Laurent P, Vita N;
XX XX
XX DR WPI; 1997-319773/29.
XX DR N-PSDB; AAT85826, AAT86464.
XX XX
XX PT New purified human interleukin-13 receptors - and related nucleic
XX PT acids, useful for diagnosis and treatment of inflammation, allergy,
XX PT etc
XX XX
XX PS Claim 1; Figure 2a; 83pp; French.
XX CC This sequence represents interleukin-13 (IL-13) beta receptor. The
XX CC invention relates to new purified peptides comprising 380 or 427 amino
XX CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
XX CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
XX CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
XX CC affinity, but acquires high affinity when associated with the IL-4
XX CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
XX CC diagnostic probes to identify aberrant synthesis or genetic anomalies
XX CC such as loss of heterozygosity and rearrangements, or chromosomal
XX CC anomalies. They are also used for production of recombinant IL-13R beta
XX CC and alpha which can be used as IL-13 antagonists, specifically to
XX CC regulate IL-13-induced responses for treatment of inflammation and
XX CC allergy. IL-13 receptors are also useful as antisense molecules for gene
XX CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
XX CC immunassays) to diagnose diseases associated with abnormal expression
XX CC of IL-13 receptors; when coupled to a toxin also for treatment of
XX CC overproduction of IL-13R. Cells that express IL-13R at the surface are
XX CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta
XX CC is encoded by the nucleic acid sequence shown in Figure 2a in the
XX CC specification (AAT86464), which is not the same as that shown in the
XX CC sequence listing (AAT85828).
XX XX
XX SQ Sequence 380 AA;
XX
XX Query Match 70.5%; Score 1503; DB 18; Length 380;
XX Best Local Similarity 72.9%; Pred No. 3.3e-137;
XX Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;
XX
QY 1 MAFIHLVDGFLYTLVCTAFG-SMLSNAEIKVNPQDFEIVDPGYLGLSLQWQPPLEPD 59
DB 1 mafvclalgcltyflistftgctssadtckvnpqdfvdpvglylylqwqpplslid 60
QY 60 NPEKCTIEYELKYRIDSNNWTITKLNHYKDGDLNKGIEAKNTLLPAOCTNGSEVR 119
DB 61 hkectvvelkyrnigsetwtiitknlhykgdglndkgleakhtllpwqctngsevg 120
QY 120 SSWAETTYTSPQGNRETKIQDMDCVYNNQYLVCSPKPGMGVHFDNTYQLEFYVWEGLDH 179
DB 121 ssaettytwispqgipetkvqmdcdvynwqyllylcswpqgpgvlltdtnynllfywyeqlh 180
QY 180 SAECTDYIKVNGKNMGCRPPYLESSDYKDFYICVNGSSSQRPFSYFYFQLQNVKPM 239
DB 181 alqcvdylkadgnglgrcfyleasdykdfyicvngssenkpirsyyfqlqnvkplp 240
QY 240 PLYLSLVKNSSEINLKNWPKGPIPAKCFYIEIFTEGDTWTVTVTVEVNETQIRTSNE 299
DB 241 pylvltfressceiklksaipgiparcfdyeleiredtdtlvtatvenetytlktne 300
QY 300 SOKLCFLVRSKVNIYCSDDGIWSESDQCKWG-DTWKETLVFELIPPAFVSIFVLVIFC 358
DB 301 trqlcfvvrskvnylcsddgiwsewskqcgwedlskktllrflwpfgfllilvifvq 360
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```
QY 359 LLLYKQKRALTKTI 371
DB 361 llllrkptntypkml 373
RESULT 9
AAW35295
ID AAW35295 standard; Protein; 380 AA.
XX AC AAW35295;
XX XX
XX DT 27-MAR-1998 (first entry)
XX XX
XX DE Human IL-13 binding chain of the IL-13 receptor.
XX KW Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;
XX KW mediator; IL-13 receptor binding inhibition; Ige-mediated condition;
XX KW allergy; asthma; immune complex disorder.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..25
XX FT /label= signal_sequence
XX FT /note= "putative"
XX FT Protein 26..380
XX FT /label= mature_protein
XX FT Domain 26..341
XX FT /label= extracellular_domain
XX FT Domain 342..362
XX FT /label= transmembrane_domain
XX FT Domain 363..380
XX FT /label= intracellular_domain
XX PN WO9731946-A1.
XX XX
XX PD 04-SEP-1997.
XX XX
XX PF 28-FEB-1997; 97WO-US03124.
XX XX
XX PR 01-MAR-1996; 96US-0609572.
XX XX
XX PA (GENY ) GENETICS INST INC.
XX PI Collins M, Donaldson D, Fitz L, Neben T, Whitters M;
XX PI Wood C;
XX XX
XX DR WPI; 1997-448632/41.
XX DR N-PSDB; AAT95214.
XX XX
XX PT New nucleic acid encoding interleukin-13 receptor binding chain and
XX PT transformed cells - proteins, antibodies and inhibitors, for
XX PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,
XX PT and in diagnosis
XX XX
XX PS Claim 11; Pages 34-35; 49pp; English.
XX XX
XX CC The present sequence represents the human interleukin-13 (IL-13) binding
XX CC chain of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
XX CC mediator of the known biological activities of IL-13. Recombinant
XX CC IL-13bc proteins, and antibodies raised against them, are used to
XX CC inhibit the binding of IL-13 to its receptor. They are particularly used
XX CC to treat Ige-mediated conditions, e.g. allergy, asthma and immune complex
XX CC disorders, especially lupus, nephritis, thyroiditis and Grave's disease.
XX CC They are also used to treat immune deficiency (particularly in .
XX CC haematopoietic progenitor cells), cancer etc., and to increase macrophage
XX CC activation, e.g. in vaccination. To potentiate IL-13 activity, a protein
XX CC with such activity is combined with IL-13bc and the mixture applied,
XX CC in vivo, to a cell expressing at least one chain of the IL-13 receptor
XX CC other than IL-13bc. IL-13bc can also be used in diagnosis to detect
XX CC expression of IL-13, its receptor or binding chain, and to raise specific
XX CC antibodies which may be useful for treating some tumours.
XX XX
```



```

SQ Sequence 380 AA;
Query Match 70.5%; Score 1503; DB 18; Length 380;
Best Local Similarity 72.9%; Pred. No. 3.3e-137;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

Qy 1 MAFIHLVDGFLYTLVLCVAFG-SMLSNAEIKVNPQDFEIVDPGVLGYLSLQWQPLFPD 59
Db 1 mafvclaigclytflistfgctssdteikvnpqdfeidvpgylglylqwqpplslid 60

Qy 60 NFKECTIEYELKYRNIDSENWKTITKNLHYKDGFDLNGKIEAKINTLLPAOCTNGSEVR 119
Db 61 hflectveyelkrynigsetwtiitknlnhykgdgdlnkgleakhtllpwqctngsevg 120

Qy 120 SSWAETTYWTSPOGNRETKIODMDCVYNNWOYLVCSSWPKGMGVHFDNTNYQLFYWYEGLDH 179
Db 121 sswaettywispqgipetkvqmdcvynwqyllicswkpgigvldtynllyfwyegldh 180

Qy 180 SAECTDYIKVNGKNGCRFPYLESSDYKDFYICVNGSSESQPIRPSYFIFOLQNIKVPMP 239
Db 181 alqcvdyikadgnigrcfyleasdykdfyicvngssenkprrsyffqlqnlvklp 240

Qy 240 PDYLSLTVKNSEENLKNWMPKGPPIAKCFIYEIEFTEDGTTWTTTVEINEIQITRTSNE 299
Db 241 pvyiltftressceiklkwsiplgiparcdyefeiaredtdtlvtatvenetytlktne 300

Qy 300 SOKLCFLYRSKVNICYSDGIIWSEWSDEOCWKG-DIWKETLVFFLTPFAFVSIFVLVITC 358
Db 301 trqlcfvrvskvniycsddgiwsewsdkqwedlskktllrfwlpfgfllilvifvtg 360

Qy 359 LLLYKQALLKTI 371
Db 361 lllrkpntypkmi 373

RESULT 10
ID AAW36613 standard; Protein; 380 AA.
AC AAW36613;
XX
XX 30-MAR-1998 (first entry)
XX Human zcytor2 cytokine receptor protein.
XX
XX Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
XX infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 340..363
XX /label= transmembrane_domain
XX Domain 364..380
XX /label= intracellular_domain
XX Domain 25..339
XX /label= ligand_binding_domain
XX
XX WO9733913-A1.
XX
XX 18-SEP-1997.
XX
XX 12-MAR-1997; 97WO-US04043.
XX
XX 13-MAR-1996; 96US-0013345.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
XX O'Hara PJ;
XX
XX WPI; 1997-470820/43.

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DR N-PSDB; AAT96782.
XX New nucleic acid encoding testis-specific cytokine receptor - useful
PT for identification of ligands or antagonists, potentially for use as
PT male contraceptives or for infertility treatment
XX
XX Claim 2; Page 47-48; 79pp; English.
XX
XX This sequence represents a novel ligand-binding receptor, zcytor2,
CC which shares homology with cytokine receptors and was isolated from human
CC placental polyA+ RNA. The resulting polypeptide is a receptor for
CC cytokines (particularly interleukin-13) and is expressed on the surface
CC of testicular cells, probably being involved in spermatogenesis. It can
CC be used to detect ligands that promote proliferation and/or
CC differentiation of such cells in culture and may also be used to treat
CC infertility. Antagonists of this receptor may be used to characterise
CC ligand-receptor interactions and as male-specific contraceptives. By
CC blocking the action of IL-13, receptor antagonists and ligand-binding
CC this receptor can also be used to modulate immune function, e.g. in
CC allergy and asthma, as a diagnostic to determine circulating levels of
CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonist.
XX
SQ Sequence 380 AA;
Query Match 70.5%; Score 1503; DB 18; Length 380;
Best Local Similarity 72.9%; Pred. No. 3.3e-137;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

Qy 1 MAFIHLVDGFLYTLVLCVAFG-SMLSNAEIKVNPQDFEIVDPGVLGYLSLQWQPLFPD 59
Db 1 mafvclaigclytflistfgctssdteikvnpqdfeidvpgylglylqwqpplslid 60

Qy 60 NFKECTIEYELKYRNIDSENWKTITKNLHYKDGFDLNGKIEAKINTLLPAOCTNGSEVR 119
Db 61 hflectveyelkrynigsetwtiitknlnhykgdgdlnkgleakhtllpwqctngsevg 120

Qy 120 SSWAETTYWTSPOGNRETKIODMDCVYNNWOYLVCSSWPKGMGVHFDNTNYQLFYWYEGLDH 179
Db 121 sswaettywispqgipetkvqmdcvynwqyllicswkpgigvldtynllyfwyegldh 180

Qy 180 SAECTDYIKVNGKNGCRFPYLESSDYKDFYICVNGSSESQPIRPSYFIFOLQNIKVPMP 239
Db 181 alqcvdyikadgnigrcfyleasdykdfyicvngssenkprrsyffqlqnlvklp 240

Qy 240 PDYLSLTVKNSEENLKNWMPKGPPIAKCFIYEIEFTEDGTTWTTTVEINEIQITRTSNE 299
Db 241 pvyiltftressceiklkwsiplgiparcdyefeiaredtdtlvtatvenetytlktne 300

Qy 300 SOKLCFLYRSKVNICYSDGIIWSEWSDEOCWKG-DIWKETLVFFLTPFAFVSIFVLVITC 358
Db 301 trqlcfvrvskvniycsddgiwsewsdkqwedlskktllrfwlpfgfllilvifvtg 360

Qy 359 LLLYKQALLKTI 371
Db 361 lllrkpntypkmi 373

RESULT 11
AAW41520
ID AAW41520 standard; Protein; 380 AA.
XX
XX AAW41520;
XX
XX 22-JUN-1998 (first entry)
XX Human HR-1 receptor.
XX
XX HR-1 receptor; human; cytokine; infection; asthma; allergy;
XX haematopoietic disorder; tumour; therapy; diagnosis.
XX
KW

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```
OS Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..21
XX Protein 22..380
XX /label= Sig_peptide
XX /label= Mat_protein
XX WO9747741-A1.
XX
XX 18-DEC-1997.
XX
XX 12-JUN-1996; 96WO-US10262.
XX
XX 12-JUN-1996; 96WO-US10262.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Appelbaum ER, Hu J;
XX
XX WPI: 1998-052308/05.
XX N-PSDB; AAV04131.
XX
XX Nucleic acid sequence encoding human cytokine peptide hormone
XX receptor - useful to treat, prevent or diagnose, e.g. lowered
XX resistance to infection, asthma, allergy or haematopoietic disease
XX
XX Claim 13; Page 62-64; 76pp; English.
XX
XX This protein comprises a novel human cytokine/peptide hormone
XX receptor, designated the HR-1 receptor, that shows 27% identity
XX and 52% similarity to the interleukin-5 receptor. Its amino acid
XX sequence was deduced from a cDNA clone (see AAV04131) obtained from a
XX human testis library. Recombinant HR-1 receptor can be expressed
XX in claimed host cells, and used in a claimed method for identifying
XX compounds which bind to, and activate or inhibit, it. HR-1
XX receptor activators and agonists can be used to treat, prevent or
XX diagnose predisposition to lowered resistance to infection, asthma,
XX allergic or haematopoietic disorders, e.g. where induced by AIDS,
XX aplastic anaemia, neutropaenia or cytotoxic treatments for cancer.
XX HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can
XX be used to treat conditions associated with HR-1 receptor
XX overexpression. The antibodies can also be used to determine HR-1
XX receptor levels, since overexpression may be diagnostic of tumours.
XX
XX Sequence 380 AA;
XX
XX Query Match 70.5%; Score 1503; DB 19; Length 380;
XX Best Local Similarity 72.9%; Pred. No. 3.3e-137;
XX Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;
XX
XX 1 MAFIHLDVGLYTLVCTAFG-SMISNAEIKVNPQDFEIVDPGYLGLVSLQWQPPLPDP 59
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 1 mafvclalgcltyflsttfgctssdssteikvnpqdfvdpgylylqwpplslid 60
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 60 NEKECTIEVELKYRNIDSENWKTITKLNHYKDGFDLNGKIEAKINTLLPAQCTNGSEVR 119
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 61 hfkectvvelkyrnlgsetwtitknlhykgdgdlnkgieakhtlllpwqctngsevg 120
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 120 SSWAETTYWTSPOGNETRIQDMDCVYVYNNQYLVCWSKPGMGVHFTNYQLFYWYEGLDH 179
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 121 sswaettywispqgipetkvqmdcvynwqylcskpgigvldntnlyfwyegldh 180
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 180 SNAECTDYIKVKNKMGCRPPYLESSDYKDFYICVNGSSSQPIRPSYFTFQLQNIYKPM 239
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 181 alqcdvdykdgngnlgcrfyleasdykdfyicvngsssenkplrassyftfqlqniwkpl 240
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 240 PLYLSITVKNSEINLKNWPKGPIPAKCFIYEIEFTEDGTTWTTVTVNEIQTITSNE 299
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 241 pylvltfressceiklkwseipgiparcfdyeleireddttlvatvenetytiktne 300
XX : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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```
QY 300 SOKLCFLVRSKVNIYCSDDGIWSEMSDEOCWKG-DIWKETLVFFELIPFAVSIFVLVITC 358
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 301 trqlcfvrvskvniycsddgiwsewskqcgwedlskktllrfwlpfgfllilvifvvg 360
QY 359 LLLLYKORALLKTI 371
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 361 llllrkpnrypkm 373

RESULT 12
AAW41502
ID AAW41502 standard; Protein; 380 AA.
XX
XX AAW41502;
XX
XX 08-JUN-1998 (first entry)
XX
XX Human cytokine/peptide receptor, HR-1 receptor.
XX
XX HR-1 receptor; cytokine receptor; peptide hormone receptor; human;
XX infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;
XX neutropaenia; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX Protein 22..380
XX /label= Sig_peptide
XX /label= Mat_protein
XX /note= "Claim 14"
XX
XX EP812913-A2.
XX
XX 17-DEC-1997.
XX
XX 04-JUN-1997; 97EP-0303815.
XX
XX 12-JUN-1996; 96US-0017843.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Appelbaum ER, Hu J;
XX
XX WPI: 1998-034974/04.
XX N-PSDB; AAV04075.
XX
XX Human cytokine/peptide hormone receptor, HR-1 receptor - useful to
XX increase resistance to infections in individuals with trauma and/or
XX burns
XX
XX Claim 13; Page 27-28; 34pp; English.
XX
XX This protein comprises a novel human cytokine/peptide hormone
XX receptor, designated HR-1 receptor. The amino acid sequence
XX was deduced from a cDNA clone (see AAV04075) isolated from a human
XX testis cDNA library. It shows 27% amino acid identity and 52%
XX similarity with the human interleukin-5 receptor. Also claimed are
XX polynucleotides encoding HR-1 receptor, vector and host cells, an
XX agonist to the polypeptide, antibody against the polypeptide, an
XX antagonist that inhibits the activity of the polypeptide, a process
XX for diagnosing a disease, or a susceptibility to disease, related
XX to expression of HR-1 receptor, and a method for identifying
XX compounds that activate or inhibit the HR-1 receptor. HR-1
XX receptor protein and polynucleotides can be used for research,
XX biological, diagnosis and (gene) therapy applications, e.g. to
XX increase resistance to infections in individuals with trauma and/or
XX burns, and to prevent, ameliorate, treat, diagnose and/or determine
XX predisposition to asthma, allergic disorders or disorders of
XX haematopoiesis induced by AIDS, aplastic anaemia, congenital or
XX cyclic neutropaenia or as a consequence of cytotoxic therapy of
```

CC	cancer, lymphoma, leukaemia and/or bone marrow transplantation.
XX	
SQ	Sequence 380 AA;
Query Match 70.5%; Score 1503; DB 19; Length 380;	
Best Local Similarity 72.9%; Pred. No. 3.3e-137;	
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;	
Qy	1 MAFIHLVDGFLYTLVCTAFG-SMLSNAEIKVNPQDFEIVDPGVLGVLQWQPLPFPD 59
Db	1 mafvclaigcyltflistfctssdteikvnpqdfvdpvglylqwpplslid 60
Qy	60 NFKECTIEYELKYRNIDSENWKTITTKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVR 119
Db	61 hfkectveyelkyrnigsetwtiitknlhkgdgdlnkgleakhtllpwqctngsevg 120
Qy	120 SSWAETTYWTSPQGNRETKIQDMDCVYVNWQYLVCWSKPGMVGHFDTNVLFWYEGLDH 179
Db	121 sswaettywispqgipeckvqmdcvynwqylcswkpgigvllidtnynlfwyegldh 180
Qy	180 SAECTDYIKVNGKNGCRFPYLESSDYKDFYICVNGSSSQPIRPSYFIFQNLIVKPM 239
Db	181 alqcvdyikadqngicrfpyleasdykdfyicvngssenkprrsyftfqlqnvkplp 240
Qy	240 PDLVSLTVKNSSEINLKNWMPKGPPIAKCFIYEIETEDGTWVTVEINEIQTITSNE 299
Db	241 pylvltressceiklkwsiplgiparcfdyeieireddtlvtatvenetytiktne 300
Qy	300 SOKLCFLVRSKVIYCSDDGIWSEWSDEQCKWG-DIWKETLVFFLIPFAFVSIFVLVITC 358
Db	301 trqlcfcvrvskvniycsddgiwsewsdkqwegedlskktllrflwlpfgfllilvifvtg 360
Qy	359 LLLYKORALLKTI 371
Db	361 lllrkptnypkmi 373
RESULT 13	
AAW33603	
ID	AAW33603 standard; Protein; 380 AA.
XX	
AC	AAW33603;
XX	
DT	08-JUN-1998 (first entry)
XX	
DE	Homo sapiens HR-1 receptor.
XX	
KW	Cytokine; hormone receptor; AIDS; acquired immune deficiency;
KW	syndrome; aplastic anaemia; neutropaenia; cancer treatment;
KW	infection resistance; diagnosis; tumours; HR-1 receptor;
KW	asthma; allergic; haematopoietic; disorder.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..21
FT	/note= "signal peptide"
XX	
PN	W09747742-A1.
XX	
PD	18-DEC-1997.
XX	
XX	
PF	09-JUL-1996; 96WO-US11459.
XX	
PR	12-JUN-1996; 96WO-US10262.
PR	12-JUN-1996; 96US-0017843.
XX	
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	(SMK) SMITHKLINE BEECHAM CORP.
XX	
PI	Appelbaum ER, Hu J;
XX	

DR	WPI; 1998-052309/05.
DR	N-PSDB; AAV02295.
XX	
PT	DNA encoding human cytokine-peptide hormone receptor - useful for
PT	treating preventing or diagnosing, e.g. lowered resistance to
XX	infection, asthma, allergy, or haematopoietic disease
PS	Claim 15; Fig 1; 75pp; English.
XX	
CC	The sequence is that of the human cytokine/peptide hormone receptor
CC	(HR-1 receptor). This, or it's activators or agonists, can be used to
CC	treat, prevent or diagnose predisposition to lowered resistance to
CC	infection, asthma, allergic or haematopoietic disorders, e.g. where
CC	induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
CC	neutropaenia or cytotoxic treatments for cancer. Antagonists of the
CC	receptor, e.g. antibodies or fragments of it may be used to treat
CC	conditions associated with overexpression of the HR-1 receptor, e.g.
CC	those listed above. Antibodies may also be used to assay levels of HR-1
CC	receptor, overexpression of which may be diagnostic of tumours, by usual
CC	immunassays; to isolate and identify HR-1 receptor-expressing cells; or
CC	for affinity purification of the HR-1 receptor.
XX	
SQ	Sequence 380 AA;
Query Match 70.5%; Score 1503; DB 19; Length 380;	
Best Local Similarity 72.9%; Pred. No. 3.3e-137;	
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;	
Qy	1 MAFIHLVDGFLYTLVCTAFG-SMLSNAEIKVNPQDFEIVDPGVLGVLQWQPLPFPD 59
Db	1 mafvclaigcyltflistfctssdteikvnpqdfvdpvglylqwpplslid 60
Qy	60 NFKECTIEYELKYRNIDSENWKTITTKNLHYKDGFDLNGKIEAKINTLLPAQCTNGSEVR 119
Db	61 hfkectveyelkyrnigsetwtiitknlhkgdgdlnkgleakhtllpwqctngsevg 120
Qy	120 SSWAETTYWTSPQGNRETKIQDMDCVYVNWQYLVCWSKPGMVGHFDTNVLFWYEGLDH 179
Db	121 sswaettywispqgipeckvqmdcvynwqylcswkpgigvllidtnynlfwyegldh 180
Qy	180 SAECTDYIKVNGKNGCRFPYLESSDYKDFYICVNGSSSQPIRPSYFIFQNLIVKPM 239
Db	181 alqcvdyikadqngicrfpyleasdykdfyicvngssenkprrsyftfqlqnvkplp 240
Qy	240 PDLVSLTVKNSSEINLKNWMPKGPPIAKCFIYEIETEDGTWVTVEINEIQTITSNE 299
Db	241 pylvltressceiklkwsiplgiparcfdyeieireddtlvtatvenetytiktne 300
Qy	300 SOKLCFLVRSKVIYCSDDGIWSEWSDEQCKWG-DIWKETLVFFLIPFAFVSIFVLVITC 358
Db	301 trqlcfcvrvskvniycsddgiwsewsdkqwegedlskktllrflwlpfgfllilvifvtg 360
Qy	359 LLLYKORALLKTI 371
Db	361 lllrkptnypkmi 373
RESULT 14	
AAAY95296	
ID	AAAY95296 standard; Protein; 380 AA.
XX	
AC	AAAY95296;
XX	
DT	12-SEP-2000 (first entry)
XX	
DE	IL-13 binding chain of human IL-13 receptor.
XX	
KW	Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW	cytokine receptor; haematopoietin receptor; atopy; allergy; asthma;
KW	immune complex disease; lupus; nephritis; thyroiditis;
KW	Grave's disease; inflammatory; infection; therapy; antiallergic;
KW	antiinflammatory; antiasthmatic; vaccine.

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..25 /note= "signal peptide"
 FT Protein 26..380 /note= "mature protein"
 FT Domain 26..341 /note= "extracellular domain; a polypeptide comprising amino acids 22-334 is specifically claimed in Claim 11(e)"
 FT Domain 342..362 /note= "transmembrane domain"
 FT Domain 363..380 /note= "intracellular domain; a polypeptide comprising amino acids 257-383 is specifically claimed in Claim 11(f)"
 XX WO2000036103-A1.
 XX 22-JUN-2000.
 PF 13-DEC-1999; 99WO-US29493.
 PR 14-DEC-1998; 98US-0211335.
 XX (GENY) GENETICS INST INC.
 PA (UJO) UNIV JOHNS HOPKINS.
 XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;
 PI Willis-Karp M;
 XX WPI: 2000-431587/37.
 DR N-PSDB; AA27912.
 XX New polynucleotide encoding an interleukin-13 (IL-13) binding chain of an IL-13 receptor for treating IgE-mediated conditions, such as atopy, asthma, Grave's disease and inflammatory conditions of the lung -
 PT Claim 11(d); Page 53-54; 60pp; English.
 XX The present sequence is that of the interleukin-13 binding chain (IL-13bc) of the human IL-13 receptor, as deduced from an isolated human testis cDNA clone (see AAA27912). IL-13bc is a member of the haematopoietin receptor family that acts as a mediator of IL-13. The invention provides methods for the recombinant production of IL-13bc polypeptides, including claimed full-length IL-13bc, its extracellular domain, and its intracellular domain. IL-13bc polypeptides, particularly soluble IL-13bc polypeptides, and IL-13 receptor inhibitors (e.g. antagonists of the interaction of IL-13 and its receptor) can be used to treat conditions in which IL-13 is implicated, particularly IgE-mediated conditions and diseases including atopy, allergy, asthma, immune complex diseases (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis, thyroiditis and Grave's disease), lung inflammation, immunodeficiency, and cancer. Since IL-13 inhibits macrophage activation, IL-13bc proteins can also be used to enhance macrophage activation, e.g. in vaccination, treatment of mycobacterial or intracellular organisms or parasite infections. IL-13bc proteins may also be used to potentiate the effects of IL-13 in vitro and in vivo, as diagnostic agents, and to screen for agents capable of binding to IL-13bc or IL-13 receptor, or which interfere with the binding of IL-13 to its receptor.
 XX Sequence 380 AA;
 SQ

Query Match 70.5%; Score 1503; DB 21; Length 380;
 Best Local Similarity 72.9%; Pred. No. 3.3e-137;
 Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;
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 QY 60 NFEKCTIEYELKYNIDSENWKTITKNLHYKDGDLNKGIEAKINTLLPAOCTNGSEVR 119
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 361 llllrkptypkmi 373
 RESULT 15
 AAG63812
 ID AAG63812 standard; Protein; 380 AA.
 AC AAG63812;
 XX 29-OCT-2001 (first entry)
 DE Amino acid sequence of human interleukin-13 receptor subunit alpha 2.
 KW Human; interleukin-13 receptor subunit alpha 2; IL-13ralpha2; cancer;
 KW testis antigen; immune response; glioma cell.
 XX Homo sapiens.
 OS WO200158479-A1.
 PN 16-AUG-2001.
 PD 08-FEB-2001; 2001WO-US04384.
 PF 08-FEB-2000; 2000US-0181000.
 PR (PENN-) PENN STATE RES FOUND.
 PA Debinski W;
 PI WPI: 2001-522435/57.
 DR N-PSDB; AAH74791.
 DR Stimulating immune response against interleukin-13 receptor alpha2 subunit in a subject having or at risk of developing gliomas, involves formulating a vaccine comprising an agent that stimulates immune response against the subunit -
 PT Claim 3; Fig 1; 66pp; English.
 XX The present sequence represents a human interleukin-13 receptor subunit alpha 2 (IL-13ralpha2), which is a cancer/testis antigen. The specification describes a method for stimulating immune response against IL-13ralpha2 subunit. The method is used for stimulating immune response against IL-13ralpha2 in a human being having or at risk of developing a cancer having glioma cells expressing IL-13ralpha2. The polypeptides and polynucleotides are useful for preventing and/or treating cancers e.g., high grade gliomas (HGG).

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XX
SQ Sequence 380 AA;

Query Match 70.5%; Score 1503; DB 22; Length 380;
Best Local Similarity 72.9%; Pred. No. 3.3e-137;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;

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